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(54) Title: PROTEASES AND ASSOCIATED PROTEINS			
(57) Abstract			
The invention provides human proteases and associated proteins (PPRG) and polynucleotides which identify and encode PPRG. The invention also provides expression vectors, host cells, antibodies, agonists, and antagonists. The invention also provides methods for diagnosing, treating, or preventing disorders associated with expression of PPRG.			

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PROTEASES AND ASSOCIATED PROTEINS

TECHNICAL FIELD

5 This invention relates to nucleic acid and amino acid sequences of proteases and associated proteins and to the use of these sequences in the diagnosis, treatment, and prevention of cell proliferative and immune disorders.

BACKGROUND OF THE INVENTION

10 Proteolytic processing is an essential component of normal cell growth, differentiation, remodeling, and homeostasis. The cleavage of peptide bonds within cells is necessary for the maturation of precursor proteins to their active forms, the removal of signal sequences from targeted proteins, the degradation of incorrectly folded proteins, and the controlled turnover of peptides within the cell. Proteases participate in apoptosis, inflammation, and tissue remodeling
15 during embryonic development, wound healing, and normal growth. They are necessary components of bacterial, parasitic, and viral invasion and replication within a host. Four principal categories of mammalian proteases have been identified based on active site structure, mechanism of action, and overall three-dimensional structure. (See Beynon, R.J. and J.S. Bond (1994) Proteolytic Enzymes: A Practical Approach, Oxford University Press, New York NY, pp. 1-5.)

20 The serine proteases (SPs) are a large family of proteolytic enzymes that include the digestive enzymes, trypsin and chymotrypsin; components of the complement cascade and of the blood-clotting cascade; and enzymes that control the degradation and turnover of macromolecules of the extracellular matrix. SPs are so named because of the presence of a serine residue in the active site for catalysis of protein cleavage. The active site of an SP is composed of a triad of
25 residues including the aforementioned serine, an aspartate, and a histidine residue. SPs have a wide range of substrate specificities and can be subdivided into subfamilies on the basis of these specificities. The main sub-families are trypases which cleave after arginine or lysine; aspases which cleave after aspartate; chymases which cleave after phenylalanine or leucine; metases which cleavage after methionine; and serases which cleave after serine. Clp protease is a unique member
30 of the serine protease family as its activity is controlled by a regulatory subunit that binds and hydrolyzes ATP. Clp protease was originally found in plant chloroplasts but is believed to be widespread in both prokaryotic and eukaryotic cells (Maurizi, M.R. et al. (1990) J. Biol. Chem. 265:12546-12552). SKD3, a mammalian homolog of the bacterial Clp regulatory subunit, has recently been identified in mouse (Perier, F. et al. (1995) Gene 152:157-163).

Cysteine proteases are involved in diverse cellular processes ranging from the processing of precursor proteins to intracellular degradation. Mammalian cysteine proteases include lysosomal cathepsins and cytosolic calcium activated proteases, calpains. Of particular note, cysteine proteases are produced by monocytes, macrophages and other cells of the immune system which migrate to sites of inflammation and, in their protective role, secrete various molecules to repair damaged tissue. These cells may overproduce the same molecules and cause tissue destruction in certain disorders. In autoimmune diseases such as rheumatoid arthritis, the secretion of the cysteine protease, cathepsin C, degrades collagen, laminin, elastin and other structural proteins found in the extracellular matrix of bones. The cathepsin family of lysosomal proteases includes the cysteine proteases: cathepsins B, H, K, L, O2, and S; and the aspartyl proteases: cathepsins D and G. Various members of this endosomal protease family are differentially expressed. Some, such as cathepsin D, have a ubiquitous tissue distribution while others, such as cathepsin L, are found only in monocytes, macrophages, and other cells of the immune system.

Aspartic proteases include bacterial penicillopepsin, mammalian pepsin, renin, chymosin, and certain fungal proteases. The characteristic active site residues of aspartic proteases are a pair of aspartic acid residues, for example, Asp33 and Asp213 in penicillopepsin. Aspartic proteases are also called acid proteases because the optimum pH for their activity is between 2 and 3. In this pH range, one of the aspartate residues is ionized and the other is neutral. A potent inhibitor of aspartic proteases is the hexapeptide pepstatin which, in the transition state, resembles normal substrates.

Carboxypeptidases A and B are the principal mammalian representatives of the metalloprotease family. Both are exopeptidases of similar structure and active site configuration. Carboxypeptidase A, like chymotrypsin, prefers C-terminal aromatic and aliphatic side chains of hydrophobic nature, whereas carboxypeptidase B is directed toward basic arginine and lysine residues. Active site components include zinc, which coordinates one histidine and two glutamic acid residues in the protein.

Proteasomes and ubiquitin proteases are both associated with the ubiquitin conjugation system (UCS), a major pathway for the degradation of cellular proteins in eukaryotic cells and some bacteria. Proteasomes are large (~2000 kDa), multisubunit complexes composed of a central catalytic core containing a variety of proteases, and terminal subunits that serve in substrate recognition and regulation of proteasome activity. The UCS mediates the elimination of abnormal proteins and regulates the half-lives of important regulatory proteins that control cellular processes such as gene transcription and cell cycle progression. In the UCS pathway, a protein targeted for

degradation is conjugated to ubiquitin, a small, heat-stable protein. The ubiquitinated protein is then recognized and degraded by a proteasome, and ubiquitin is released by ubiquitin protease for reutilization in the UCS. The UCS is implicated in the degradation of mitotic cyclic kinases, oncoproteins, tumor suppressor genes such as p53, viral proteins, cell surface receptors associated
5 with signal transduction, transcriptional regulators, and mutated or damaged proteins (Ciechanover, A. (1994) *Cell* 79:13-21). A murine proto-oncogene, Unp, encodes a nuclear ubiquitin protease whose overexpression leads to oncogenic transformation of NIH 3T3 cells, and the human homolog of this gene is consistently elevated in small cell tumors and adenocarcinomas of the lung (Gray, D.A. (1995) *Oncogene* 10:2179-2183).

10 Many other proteolytic enzymes do not fit any of the major categories discussed above because their mechanisms of action and/or active sites have not been elucidated. These include the aminopeptidases and signal peptidases. Aminopeptidases catalyze the hydrolysis of amino acid residues from the amino terminus of peptide substrates. Bovine leucine aminopeptidase is a zinc metalloenzyme that utilizes the sulfhydryl groups from at least three reactive cysteine
15 residues at its active site in the binding of metal ions (Cuypers, H.T. et al. (1982) *J. Biol. Chem.* 257:7086-7091).

Signal peptidases are a specialized class of proteases found in all prokaryotic and eukaryotic cell types that serve in the processing of signal peptides. Signal peptides are amino-terminal sequences which direct the protein from its ribosomal assembly site to a particular
20 cellular or extracellular location. Once the protein has been exported, removal of the signal sequence by a signal peptidase and posttranslational processing activate the protein. Signal peptidases exist as multi-subunit complexes in both yeast and mammals.

Protease inhibitors and other regulators of protease activity control the activity and effects of proteases. Protease inhibitors have been shown to control pathogenesis in animal models of
25 proteolytic disorders (Murphy, G. (1991) *Agents Actions Suppl.* 35:69-76). Low levels of the cystatins, low molecular weight inhibitors of the cysteine proteases, correlate with malignant progression of tumors. (Calkins, C. et al. (1995) *Biol. Biochem. Hoppe Seyler* 376:71-80). Also, increases in cysteine protease levels, when accompanied by reductions in inhibitor activity, are correlated with the pathology of arthritis and immunological diseases in humans.

30 Serpins are inhibitors of mammalian plasma serine proteases. Many serpins serve to regulate the blood clotting cascade and/or the complement cascade in mammals. Sp32 is a positive regulator of the mammalian acrosomal protease, acrosin. Sp32 binds the proenzyme, proacrosin, and thereby aides in packaging the enzyme into the acrosomal matrix (Baba, T. et al. (1994) *J. Biol. Chem.* 269:10133-10140).

The Kunitz family of serine protease inhibitors is characterized by one or more "Kunitz domains" containing a series of cysteine residues that are regularly spaced over approximately 50 amino acid residues and form three intrachain disulfide bonds. Members of this family include aprotinin, tissue factor pathway inhibitor (TFPI-1 and TFPI-2), inter- α -trypsin inhibitor, and
5 bikunin (Marlor, C.W. et al. (1997) J. Biol. Chem. 272:12202-12208). Members of this family are potent inhibitors (in the nanomolar range) against serine proteases such as kallikrein and plasmin.

The discovery of new proteases and associated proteins and the polynucleotides encoding them satisfies a need in the art by providing new compositions which are useful in the diagnosis, prevention, and treatment of cell proliferative and immune disorders.

10

SUMMARY OF THE INVENTION

The invention features substantially purified polypeptides, proteases and associated proteins referred to collectively as "PPRG" and individually as "PPRG-1," "PPRG-2," "PPRG-3," "PPRG-4," "PPRG-5," "PPRG-6," "PPRG-7," "PPRG-8," "PPRG-9," "PPRG-10," "PPRG-11,"
15 "PPRG-12," "PPRG-13," "PPRG-14," "PPRG-15," "PPRG-16," "PPRG-17," "PPRG-18," "PPRG-19," and "PPRG-20." In one aspect, the invention provides a substantially purified polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-20, and fragments thereof.

The invention further provides a substantially purified variant having at least 90% amino
20 acid identity to at least one of the amino acid sequences selected from the group consisting of SEQ ID NO:1-20 and fragments thereof. The invention also provides an isolated and purified polynucleotide encoding the polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-20 and fragments thereof. The invention also includes an isolated and purified polynucleotide variant having at least 90% polynucleotide sequence identity
25 to the polynucleotide encoding the polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-20 and fragments thereof.

Additionally, the invention provides an isolated and purified polynucleotide which hybridizes under stringent conditions to the polynucleotide encoding the polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-20 and fragments
30 thereof. The invention also provides an isolated and purified polynucleotide having a sequence which is complementary to the polynucleotide encoding the polypeptide comprising the amino acid sequence selected from the group consisting of SEQ ID NO:1-20 and fragments thereof.

The invention also provides a method for detecting a polynucleotide in a sample containing nucleic acids, the method comprising the steps of (a) hybridizing the complement of the

polynucleotide sequence to at least one of the polynucleotides of the sample, thereby forming a hybridization complex; and (b) detecting the hybridization complex, wherein the presence of the hybridization complex correlates with the presence of a polynucleotide in the sample. In one aspect, the method further comprises amplifying the polynucleotide prior to hybridization.

- 5 The invention also provides an isolated and purified polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:21-40, and fragments thereof. The invention further provides an isolated and purified polynucleotide variant having at least 90% polynucleotide sequence identity to the polynucleotide sequence selected from the group consisting of SEQ ID NO:21-40 and fragments thereof. The invention also provides an
- 10 isolated and purified polynucleotide having a sequence which is complementary to the polynucleotide comprising a polynucleotide sequence selected from the group consisting of SEQ ID NO:21-40 and fragments thereof.

- The invention further provides an expression vector containing at least a fragment of the polynucleotide encoding the polypeptide comprising an amino acid sequence selected from the
- 15 group consisting of SEQ ID NO:1-20 and fragments thereof. In another aspect, the expression vector is contained within a host cell.

- The invention also provides a method for producing a polypeptide, the method comprising the steps of: (a) culturing the host cell containing an expression vector containing at least a fragment of a polynucleotide under conditions suitable for the expression of the polypeptide; and
- 20 (b) recovering the polypeptide from the host cell culture.

 The invention also provides a pharmaceutical composition comprising a substantially purified polypeptide having the amino acid sequence selected from the group consisting of SEQ ID NO:1-20 and fragments thereof, in conjunction with a suitable pharmaceutical carrier.

- The invention further includes a purified antibody which binds to a polypeptide selected
- 25 from the group consisting of SEQ ID NO:1-20 and fragments thereof. The invention also provides a purified agonist and a purified antagonist to the polypeptide.

- The invention also provides a method for treating or preventing a disorder associated with decreased expression or activity of PPRG, the method comprising administering to a subject in need of such treatment an effective amount of a pharmaceutical composition comprising a
- 30 substantially purified polypeptide having the amino acid sequence selected from the group consisting of SEQ ID NO:1-20 and fragments thereof, in conjunction with a suitable pharmaceutical carrier.

 The invention also provides a method for treating or preventing a disorder associated with increased expression or activity of PPRG, the method comprising administering to a subject in

need of such treatment an effective amount of an antagonist of a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:1-20 and fragments thereof.

BRIEF DESCRIPTION OF THE TABLES

5 Table 1 shows polypeptide and nucleotide sequence identification numbers (SEQ ID NOs), clone identification numbers (clone IDs), cDNA libraries, and cDNA fragments used to assemble full-length sequences encoding PPRG.

Table 2 shows features of each polypeptide sequence, including potential motifs, homologous sequences, and methods and algorithms used for identification of PPRG.

10 Table 3 shows the tissue-specific expression patterns of each nucleic acid sequence as determined by northern analysis, diseases, disorders, or conditions associated with these tissues, and the vector into which each cDNA was cloned.

Table 4 describes the tissues used to construct the cDNA libraries from which cDNA clones encoding PPRG were isolated.

15 Table 5 shows the tools, programs, and algorithms used to analyze PPRG, along with applicable descriptions, references, and threshold parameters.

DESCRIPTION OF THE INVENTION

Before the present proteins, nucleotide sequences, and methods are described, it is
20 understood that this invention is not limited to the particular machines, materials and methods described, as these may vary. It is also to be understood that the terminology used herein is for the purpose of describing particular embodiments only, and is not intended to limit the scope of the present invention which will be limited only by the appended claims.

It must be noted that as used herein and in the appended claims, the singular forms "a,"
25 "an," and "the" include plural reference unless the context clearly dictates otherwise. Thus, for example, a reference to "a host cell" includes a plurality of such host cells, and a reference to "an antibody" is a reference to one or more antibodies and equivalents thereof known to those skilled in the art, and so forth.

Unless defined otherwise, all technical and scientific terms used herein have the same
30 meanings as commonly understood by one of ordinary skill in the art to which this invention belongs. Although any machines, materials, and methods similar or equivalent to those described herein can be used to practice or test the present invention, the preferred machines, materials and methods are now described. All publications mentioned herein are cited for the purpose of describing and disclosing the cell lines, protocols, reagents and vectors which are reported in the
35 publications and which might be used in connection with the invention. Nothing herein is to be

construed as an admission that the invention is not entitled to antedate such disclosure by virtue of prior invention.

DEFINITIONS

“PPRG” refers to the amino acid sequences of substantially purified PPRG obtained from
5 any species, particularly a mammalian species, including bovine, ovine, porcine, murine, equine,
and preferably the human species, from any source, whether natural, synthetic, semi-synthetic, or
recombinant.

The term “agonist” refers to a molecule which, when bound to PPRG, increases or
prolongs the duration of the effect of PPRG. Agonists may include proteins, nucleic acids,
10 carbohydrates, or any other molecules which bind to and modulate the effect of PPRG.

An “allelic variant” is an alternative form of the gene encoding PPRG. Allelic variants
may result from at least one mutation in the nucleic acid sequence and may result in altered
mRNAs or in polypeptides whose structure or function may or may not be altered. Any given
natural or recombinant gene may have none, one, or many allelic forms. Common mutational
15 changes which give rise to allelic variants are generally ascribed to natural deletions, additions, or
substitutions of nucleotides. Each of these types of changes may occur alone, or in combination
with the others, one or more times in a given sequence.

“Altered” nucleic acid sequences encoding PPRG include those sequences with deletions,
insertions, or substitutions of different nucleotides, resulting in a polynucleotide the same as PPRG
20 or a polypeptide with at least one functional characteristic of PPRG. Included within this
definition are polymorphisms which may or may not be readily detectable using a particular
oligonucleotide probe of the polynucleotide encoding PPRG, and improper or unexpected
hybridization to allelic variants, with a locus other than the normal chromosomal locus for the
polynucleotide sequence encoding PPRG. The encoded protein may also be “altered,” and may
25 contain deletions, insertions, or substitutions of amino acid residues which produce a silent change
and result in a functionally equivalent PPRG. Deliberate amino acid substitutions may be made on
the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity, and/or the
amphipathic nature of the residues, as long as the biological or immunological activity of PPRG is
retained. For example, negatively charged amino acids may include aspartic acid and glutamic
30 acid, positively charged amino acids may include lysine and arginine, and amino acids with
uncharged polar head groups having similar hydrophilicity values may include leucine, isoleucine,
and valine; glycine and alanine; asparagine and glutamine; serine and threonine; and
phenylalanine and tyrosine.

The terms “amino acid” and “amino acid sequence” refer to an oligopeptide, peptide,

polypeptide, or protein sequence, or a fragment of any of these, and to naturally occurring or synthetic molecules. In this context, "fragments," "immunogenic fragments," or "antigenic fragments" refer to fragments of PPRG which are preferably at least 5 to about 15 amino acids in length, most preferably at least 14 amino acids, and which retain some biological activity or immunological activity of PPRG. Where "amino acid sequence" is recited to refer to an amino acid sequence of a naturally occurring protein molecule, "amino acid sequence" and like terms are not meant to limit the amino acid sequence to the complete native amino acid sequence associated with the recited protein molecule.

"Amplification" relates to the production of additional copies of a nucleic acid sequence.

10 Amplification is generally carried out using polymerase chain reaction (PCR) technologies well known in the art.

The term "antagonist" refers to a molecule which, when bound to PPRG, decreases the amount or the duration of the effect of the biological or immunological activity of PPRG.

Antagonists may include proteins, nucleic acids, carbohydrates, antibodies, or any other molecules which decrease the effect of PPRG.

15 The term "antibody" refers to intact molecules as well as to fragments thereof, such as Fab, F(ab')₂, and Fv fragments, which are capable of binding the epitopic determinant. Antibodies that bind PPRG polypeptides can be prepared using intact polypeptides or using fragments containing small peptides of interest as the immunizing antigen. The polypeptide or oligopeptide used to immunize an animal (e.g., a mouse, a rat, or a rabbit) can be derived from the translation of RNA, or synthesized chemically, and can be conjugated to a carrier protein if desired. Commonly used carriers that are chemically coupled to peptides include bovine serum albumin, thyroglobulin, and keyhole limpet hemocyanin (KLH). The coupled peptide is then used to immunize the animal.

25 The term "antigenic determinant" refers to that fragment of a molecule (i.e., an epitope) that makes contact with a particular antibody. When a protein or a fragment of a protein is used to immunize a host animal, numerous regions of the protein may induce the production of antibodies which bind specifically to antigenic determinants (given regions or three-dimensional structures on the protein). An antigenic determinant may compete with the intact antigen (i.e., the immunogen used to elicit the immune response) for binding to an antibody.

30 The term "antisense" refers to any composition containing a nucleic acid sequence which is complementary to the "sense" strand of a specific nucleic acid sequence. Antisense molecules may be produced by any method including synthesis or transcription. Once introduced into a cell, the complementary nucleotides combine with natural sequences produced by the cell to form duplexes and to block either transcription or translation. The designation "negative" can refer to

the antisense strand, and the designation "positive" can refer to the sense strand.

The term "biologically active" refers to a protein having structural, regulatory, or biochemical functions of a naturally occurring molecule. Likewise, "immunologically active" refers to the capability of the natural, recombinant, or synthetic PPRG, or of any oligopeptide thereof, to induce a specific immune response in appropriate animals or cells and to bind with specific antibodies.

The terms "complementary" and "complementarity" refer to the natural binding of polynucleotides by base pairing. For example, the sequence "5' A-G-T 3'" bonds to the complementary sequence "3' T-C-A 5'." Complementarity between two single-stranded molecules may be "partial," such that only some of the nucleic acids bind, or it may be "complete," such that total complementarity exists between the single stranded molecules. The degree of complementarity between nucleic acid strands has significant effects on the efficiency and strength of the hybridization between the nucleic acid strands. This is of particular importance in amplification reactions, which depend upon binding between nucleic acids strands, and in the design and use of peptide nucleic acid (PNA) molecules.

A "composition comprising a given polynucleotide sequence" and a "composition comprising a given amino acid sequence" refer broadly to any composition containing the given polynucleotide or amino acid sequence. The composition may comprise a dry formulation or an aqueous solution. Compositions comprising polynucleotide sequences encoding PPRG or fragments of PPRG may be employed as hybridization probes. The probes may be stored in freeze-dried form and may be associated with a stabilizing agent such as a carbohydrate. In hybridizations, the probe may be deployed in an aqueous solution containing salts (e.g., NaCl), detergents (e.g., sodium dodecyl sulfate; SDS), and other components (e.g., Denhardt's solution, dry milk, salmon sperm DNA, etc.).

"Consensus sequence" refers to a nucleic acid sequence which has been resequenced to resolve uncalled bases, extended using the XL-PCR kit (Perkin-Elmer, Norwalk CT) in the 5' and/or the 3' direction, and resequenced, or which has been assembled from the overlapping sequences of more than one Incyte Clone using a computer program for fragment assembly, such as the GELVIEW fragment assembly system (GCG, Madison WI). Some sequences have been both extended and assembled to produce the consensus sequence.

The term "correlates with expression of a polynucleotide" indicates that the detection of the presence of nucleic acids, the same or related to a nucleic acid sequence encoding PPRG, by northern analysis is indicative of the presence of nucleic acids encoding PPRG in a sample, and thereby correlates with expression of the transcript from the polynucleotide encoding PPRG.

A "deletion" refers to a change in the amino acid or nucleotide sequence that results in the absence of one or more amino acid residues or nucleotides.

The term "derivative" refers to the chemical modification of a polypeptide sequence, or a polynucleotide sequence. Chemical modifications of a polynucleotide sequence can include, for example, replacement of hydrogen by an alkyl, acyl, or amino group. A derivative polynucleotide encodes a polypeptide which retains at least one biological or immunological function of the natural molecule. A derivative polypeptide is one modified by glycosylation, pegylation, or any similar process that retains at least one biological or immunological function of the polypeptide from which it was derived.

10 The term "similarity" refers to a degree of complementarity. There may be partial similarity or complete similarity. The word "identity" may substitute for the word "similarity." A partially complementary sequence that at least partially inhibits an identical sequence from hybridizing to a target nucleic acid is referred to as "substantially similar." The inhibition of hybridization of the completely complementary sequence to the target sequence may be examined
15 using a hybridization assay (Southern or northern blot, solution hybridization, and the like) under conditions of reduced stringency. A substantially similar sequence or hybridization probe will compete for and inhibit the binding of a completely similar (identical) sequence to the target sequence under conditions of reduced stringency. This is not to say that conditions of reduced stringency are such that non-specific binding is permitted, as reduced stringency conditions
20 require that the binding of two sequences to one another be a specific (i.e., a selective) interaction. The absence of non-specific binding may be tested by the use of a second target sequence which lacks even a partial degree of complementarity (e.g., less than about 30% similarity or identity). In the absence of non-specific binding, the substantially similar sequence or probe will not hybridize to the second non-complementary target sequence.

25 The phrases "percent identity" and "% identity" refer to the percentage of sequence similarity found in a comparison of two or more amino acid or nucleic acid sequences. Percent identity can be determined electronically, e.g., by using the MEGALIGN program (DNASTAR, Madison WI) which creates alignments between two or more sequences according to methods selected by the user, e.g., the clustal method. (See, e.g., Higgins, D.G. and P.M. Sharp (1988) Gene 73:237-244.) Parameters for each method may be the default parameters provided by
30 MEGALIGN or may be specified by the user. The clustal algorithm groups sequences into clusters by examining the distances between all pairs. The clusters are aligned pairwise and then in groups. The percentage similarity between two amino acid sequences, e.g., sequence A and sequence B, is calculated by dividing the length of sequence A, minus the number of gap residues

in sequence A, minus the number of gap residues in sequence B, into the sum of the residue matches between sequence A and sequence B, times one hundred. Gaps of low or of no similarity between the two amino acid sequences are not included in determining percentage similarity. Percent identity between nucleic acid sequences can also be counted or calculated by other methods known in the art, e.g., the Jotun Hein method. (See, e.g., Hein, J. (1990) *Methods Enzymol.* 183:626-645.) Identity between sequences can also be determined by other methods known in the art, e.g., by varying hybridization conditions.

“Human artificial chromosomes” (HACs) are linear microchromosomes which may contain DNA sequences of about 6 kb to 10 Mb in size, and which contain all of the elements required for stable mitotic chromosome segregation and maintenance.

The term “humanized antibody” refers to antibody molecules in which the amino acid sequence in the non-antigen binding regions has been altered so that the antibody more closely resembles a human antibody, and still retains its original binding ability.

“Hybridization” refers to any process by which a strand of nucleic acid binds with a complementary strand through base pairing.

The term “hybridization complex” refers to a complex formed between two nucleic acid sequences by virtue of the formation of hydrogen bonds between complementary bases. A hybridization complex may be formed in solution (e.g., C₀t or R₀t analysis) or formed between one nucleic acid sequence present in solution and another nucleic acid sequence immobilized on a solid support (e.g., paper, membranes, filters, chips, pins or glass slides, or any other appropriate substrate to which cells or their nucleic acids have been fixed).

The words “insertion” and “addition” refer to changes in an amino acid or nucleotide sequence resulting in the addition of one or more amino acid residues or nucleotides, respectively, to the sequence found in the naturally occurring molecule.

“Immune response” can refer to conditions associated with inflammation, trauma, immune disorders, or infectious or genetic disease, etc. These conditions can be characterized by expression of various factors, e.g., cytokines, chemokines, and other signaling molecules, which may affect cellular and systemic defense systems.

The term “microarray” refers to an arrangement of distinct polynucleotides on a substrate.

The terms “element” and “array element” in a microarray context, refer to hybridizable polynucleotides arranged on the surface of a substrate.

The term “modulate” refers to a change in the activity of PPRG. For example, modulation may cause an increase or a decrease in protein activity, binding characteristics, or any other biological, functional, or immunological properties of PPRG.

The phrases "nucleic acid" or "nucleic acid sequence," as used herein, refer to a nucleotide, oligonucleotide, polynucleotide, or any fragment thereof. These phrases also refer to DNA or RNA of genomic or synthetic origin which may be single-stranded or double-stranded and may represent the sense or the antisense strand, to peptide nucleic acid (PNA), or to any DNA-like or RNA-like material. In this context, "fragments" refers to those nucleic acid sequences which comprise a region of unique polynucleotide sequence that specifically identifies SEQ ID NO:21-40, for example, as distinct from any other sequence in the same genome. For example, a fragment of SEQ ID NO:21-40 is useful in hybridization and amplification technologies and in analogous methods that distinguish SEQ ID NO:21-40 from related polynucleotide sequences. A fragment of SEQ ID NO:21-40 is at least about 15-20 nucleotides in length. The precise length of the fragment of SEQ ID NO:21-40 and the region of SEQ ID NO:21-40 to which the fragment corresponds are routinely determinable by one of ordinary skill in the art based on the intended purpose for the fragment. In some cases, a fragment, when translated, would produce polypeptides retaining some functional characteristic, e.g., antigenicity, or structural domain characteristic, e.g., ATP-binding site, of the full-length polypeptide.

The terms "operably associated" and "operably linked" refer to functionally related nucleic acid sequences. A promoter is operably associated or operably linked with a coding sequence if the promoter controls the translation of the encoded polypeptide. While operably associated or operably linked nucleic acid sequences can be contiguous and in the same reading frame, certain genetic elements, e.g., repressor genes, are not contiguously linked to the sequence encoding the polypeptide but still bind to operator sequences that control expression of the polypeptide.

The term "oligonucleotide" refers to a nucleic acid sequence of at least about 6 nucleotides to 60 nucleotides, preferably about 15 to 30 nucleotides, and most preferably about 20 to 25 nucleotides, which can be used in PCR amplification or in a hybridization assay or microarray. "Oligonucleotide" is substantially equivalent to the terms "amplimer," "primer," "oligomer," and "probe," as these terms are commonly defined in the art.

"Peptide nucleic acid" (PNA) refers to an antisense molecule or anti-gene agent which comprises an oligonucleotide of at least about 5 nucleotides in length linked to a peptide backbone of amino acid residues ending in lysine. The terminal lysine confers solubility to the composition. PNAs preferentially bind complementary single stranded DNA or RNA and stop transcript elongation, and may be pegylated to extend their lifespan in the cell.

The term "sample" is used in its broadest sense. A sample suspected of containing nucleic acids encoding PPRG, or fragments thereof, or PPRG itself, may comprise a bodily fluid; an

extract from a cell, chromosome, organelle, or membrane isolated from a cell; a cell; genomic DNA, RNA, or cDNA, in solution or bound to a substrate; a tissue; a tissue print; etc.

The terms "specific binding" and "specifically binding" refer to that interaction between a protein or peptide and an agonist, an antibody, or an antagonist. The interaction is dependent upon the presence of a particular structure of the protein, e.g., the antigenic determinant or epitope, recognized by the binding molecule. For example, if an antibody is specific for epitope "A," the presence of a polypeptide containing the epitope A, or the presence of free unlabeled A, in a reaction containing free labeled A and the antibody will reduce the amount of labeled A that binds to the antibody.

10 The term "stringent conditions" refers to conditions which permit hybridization between polynucleotides and the claimed polynucleotides. Stringent conditions can be defined by salt concentration, the concentration of organic solvent, e.g., formamide, temperature, and other conditions well known in the art. In particular, stringency can be increased by reducing the concentration of salt, increasing the concentration of formamide, or raising the hybridization
15 temperature.

The term "substantially purified" refers to nucleic acid or amino acid sequences that are removed from their natural environment and are isolated or separated, and are at least about 60% free, preferably about 75% free, and most preferably about 90% free from other components with which they are naturally associated.

20 A "substitution" refers to the replacement of one or more amino acids or nucleotides by different amino acids or nucleotides, respectively.

"Substrate" refers to any suitable rigid or semi-rigid support including membranes, filters, chips, slides, wafers, fibers, magnetic or nonmagnetic beads, gels, tubing, plates, polymers, microparticles and capillaries. The substrate can have a variety of surface forms, such as wells,
25 trenches, pins, channels and pores, to which polynucleotides or polypeptides are bound.

"Transformation" describes a process by which exogenous DNA enters and changes a recipient cell. Transformation may occur under natural or artificial conditions according to various methods well known in the art, and may rely on any known method for the insertion of foreign nucleic acid sequences into a prokaryotic or eukaryotic host cell. The method for
30 transformation is selected based on the type of host cell being transformed and may include, but is not limited to, viral infection, electroporation, heat shock, lipofection, and particle bombardment. The term "transformed" cells includes stably transformed cells in which the inserted DNA is capable of replication either as an autonomously replicating plasmid or as part of the host chromosome, as well as transiently transformed cells which express the inserted DNA or RNA for

limited periods of time.

A "variant" of PPRG polypeptides refers to an amino acid sequence that is altered by one or more amino acid residues. The variant may have "conservative" changes, wherein a substituted amino acid has similar structural or chemical properties (e.g., replacement of leucine with isoleucine). More rarely, a variant may have "nonconservative" changes (e.g., replacement of glycine with tryptophan). Analogous minor variations may also include amino acid deletions or insertions, or both. Guidance in determining which amino acid residues may be substituted, inserted, or deleted without abolishing biological or immunological activity may be found using computer programs well known in the art, for example, LASERGENE software (DNASTAR).

10 The term "variant," when used in the context of a polynucleotide sequence, may encompass a polynucleotide sequence related to PPRG. This definition may also include, for example, "allelic" (as defined above), "splice," "species," or "polymorphic" variants. A splice variant may have significant identity to a reference molecule, but will generally have a greater or lesser number of polynucleotides due to alternate splicing of exons during mRNA processing. The
15 corresponding polypeptide may possess additional functional domains or an absence of domains. Species variants are polynucleotide sequences that vary from one species to another. The resulting polypeptides generally will have significant amino acid identity relative to each other. A polymorphic variant is a variation in the polynucleotide sequence of a particular gene between individuals of a given species. Polymorphic variants also may encompass "single nucleotide
20 polymorphisms" (SNPs) in which the polynucleotide sequence varies by one base. The presence of SNPs may be indicative of, for example, a certain population, a disease state, or a propensity for a disease state.

THE INVENTION

The invention is based on the discovery of new human proteases and associated proteins
25 (PPRG), the polynucleotides encoding PPRG, and the use of these compositions for the diagnosis, treatment, or prevention of cell proliferative and immune disorders.

Table 1 lists the Incyte clones used to assemble full length nucleotide sequences encoding PPRG. Columns 1 and 2 show the sequence identification numbers (SEQ ID NOs) of the polypeptide and nucleotide sequences, respectively. Column 3 shows the clone IDs of the Incyte
30 clones in which nucleic acids encoding each PPRG were identified, and column 4 shows the cDNA libraries from which these clones were isolated. Column 5 shows Incyte clones and their corresponding cDNA libraries. Clones for which cDNA libraries are not indicated were derived from pooled cDNA libraries. The clones in column 5 were used to assemble the consensus nucleotide sequence of each PPRG and are useful as fragments in hybridization technologies.

The columns of Table 2 show various properties of each of the polypeptides of the invention: column 1 references the SEQ ID NO; column 2 shows the number of amino acid residues in each polypeptide; column 3 shows potential phosphorylation sites; column 4 shows potential glycosylation sites; column 5 shows the amino acid residues comprising signature sequences and motifs; column 6 shows the identity of each polypeptide; and column 7 shows analytical methods used to identify each polypeptide through sequence homology and protein motifs.

The columns of Table 3 show the tissue-specificity and diseases, disorders, or conditions associated with nucleotide sequences encoding PPRG. The first column of Table 3 lists the nucleotide SEQ ID NOs. Column 2 lists tissue categories which express PPRG as a fraction of total tissue categories expressing PPRG. Column 3 lists diseases, disorders, or conditions associated with those tissues expressing PPRG. Column 4 lists the vectors used to subclone the cDNA library. Of particular note is the kidney-specific expression of SEQ ID NO:29 in 5 out of 7 libraries (71%). Also of note is expression of SEQ ID NO:34 in cervical tumor libraries (60%).

The columns of Table 4 show descriptions of the tissues used to construct the cDNA libraries from which cDNA clones encoding PPRG were isolated. Column 1 references the nucleotide SEQ ID NOs, column 2 shows the cDNA libraries from which these clones were isolated, and column 3 shows the tissue origins and other descriptive information relevant to the cDNA libraries in column 2.

The following fragments of the nucleotide sequences encoding PPRG are useful, for example, in hybridization or amplification technologies to identify SEQ ID NO:21-40 and to distinguish between SEQ ID NO:21-40 and related polynucleotide sequences. The useful fragments include the fragment of SEQ ID NO:21 from about nucleotide 1 to about nucleotide 56; the fragment of SEQ ID NO:22 from about nucleotide 161 to about nucleotide 213; the fragment of SEQ ID NO:23 from about nucleotide 110 to about nucleotide 158; the fragment of SEQ ID NO:24 from about nucleotide 117 to about nucleotide 174; the fragment of SEQ ID NO:25 from about nucleotide 191 to about nucleotide 245; the fragment of SEQ ID NO:26 from about nucleotide 204 to about nucleotide 269; the fragment of SEQ ID NO:27 from about nucleotide 181 to about nucleotide 221; the fragments of SEQ ID NO:28 from about nucleotide 509 to about nucleotide 553, and from about nucleotide 1751 to about nucleotide 1795; the fragment of SEQ ID NO:29 from about nucleotide 326 to about nucleotide 370; the fragment of SEQ ID NO:30 from about nucleotide 1190 to about nucleotide 1234; the fragment of SEQ ID NO:31 from about nucleotide 283 to about nucleotide 324; the fragment of SEQ ID NO:32 from about nucleotide 380 to about nucleotide 424; the fragments of SEQ ID NO:33 from about nucleotide 272 to about

nucleotide 316, and from about nucleotide 1784 to about nucleotide 1831; the fragment of SEQ ID NO:34 from about nucleotide 217 to about nucleotide 261; the fragment of SEQ ID NO:35 from about nucleotide 2397 to about nucleotide 2441; the fragment of SEQ ID NO:36 from about nucleotide 218 to about nucleotide 262; the fragments of SEQ ID NO:37 from about nucleotide 165 to about nucleotide 209, and from about nucleotide 651 to about nucleotide 695; the fragment of SEQ ID NO:38 from about nucleotide 812 to about nucleotide 856; the fragment of SEQ ID NO:39 from about nucleotide 541 to about nucleotide 585; and the fragment of SEQ ID NO:40 from about nucleotide 163 to about nucleotide 207. The polypeptides encoded by these fragments are useful, for example, as immunogenic peptides.

10 The invention also encompasses PPRG variants. A preferred PPRG variant is one which has at least about 80%, more preferably at least about 90%, and most preferably at least about 95% amino acid sequence identity to the PPRG amino acid sequence, and which contains at least one functional or structural characteristic of PPRG.

 The invention also encompasses polynucleotides which encode PPRG. In a particular
15 embodiment, the invention encompasses a polynucleotide sequence comprising a sequence selected from the group consisting of SEQ ID NO:21-40, which encodes PPRG.

 The invention also encompasses a variant of a polynucleotide sequence encoding PPRG. In particular, such a variant polynucleotide sequence will have at least about 80%, more preferably at least about 90%, and most preferably at least about 95% polynucleotide sequence identity to the
20 polynucleotide sequence encoding PPRG. A particular aspect of the invention encompasses a variant of a polynucleotide sequence comprising a sequence selected from the group consisting of SEQ ID NO:21-40 which has at least about 80%, more preferably at least about 90%, and most preferably at least about 95% polynucleotide sequence identity to a nucleic acid sequence selected from the group consisting of SEQ ID NO:21-40. Any one of the polynucleotide variants described
25 above can encode an amino acid sequence which contains at least one functional or structural characteristic of PPRG.

 It will be appreciated by those skilled in the art that as a result of the degeneracy of the genetic code, a multitude of polynucleotide sequences encoding PPRG, some bearing minimal similarity to the polynucleotide sequences of any known and naturally occurring gene, may be
30 produced. Thus, the invention contemplates each and every possible variation of polynucleotide sequence that could be made by selecting combinations based on possible codon choices. These combinations are made in accordance with the standard triplet genetic code as applied to the polynucleotide sequence of naturally occurring PPRG, and all such variations are to be considered as being specifically disclosed.

Although nucleotide sequences which encode PPRG and its variants are preferably capable of hybridizing to the nucleotide sequence of the naturally occurring PPRG under appropriately selected conditions of stringency, it may be advantageous to produce nucleotide sequences encoding PPRG or its derivatives possessing a substantially different codon usage, e.g.,

5 inclusion of non-naturally occurring codons. Codons may be selected to increase the rate at which expression of the peptide occurs in a particular prokaryotic or eukaryotic host in accordance with the frequency with which particular codons are utilized by the host. Other reasons for substantially altering the nucleotide sequence encoding PPRG and its derivatives without altering the encoded amino acid sequences include the production of RNA transcripts having more

10 desirable properties, such as a greater half-life, than transcripts produced from the naturally occurring sequence.

The invention also encompasses production of DNA sequences which encode PPRG and PPRG derivatives, or fragments thereof, entirely by synthetic chemistry. After production, the synthetic sequence may be inserted into any of the many available expression vectors and cell

15 systems using reagents well known in the art. Moreover, synthetic chemistry may be used to introduce mutations into a sequence encoding PPRG or any fragment thereof.

Also encompassed by the invention are polynucleotide sequences that are capable of hybridizing to the claimed polynucleotide sequences, and, in particular, to those shown in SEQ ID NO:21-40 and fragments thereof under various conditions of stringency. (See, e.g., Wahl, G.M.

20 and S.L. Berger (1987) *Methods Enzymol.* 152:399-407; Kimmel, A.R. (1987) *Methods Enzymol.* 152:507-511.) For example, stringent salt concentration will ordinarily be less than about 750 mM NaCl and 75 mM trisodium citrate, preferably less than about 500 mM NaCl and 50 mM trisodium citrate, and most preferably less than about 250 mM NaCl and 25 mM trisodium citrate. Low stringency hybridization can be obtained in the absence of organic solvent, e.g., formamide, while

25 high stringency hybridization can be obtained in the presence of at least about 35% formamide, and most preferably at least about 50% formamide. Stringent temperature conditions will ordinarily include temperatures of at least about 30°C, more preferably of at least about 37°C, and most preferably of at least about 42°C. Varying additional parameters, such as hybridization time, the concentration of detergent, e.g., sodium dodecyl sulfate (SDS), and the inclusion or exclusion

30 of carrier DNA, are well known to those skilled in the art. Various levels of stringency are accomplished by combining these various conditions as needed. In a preferred embodiment, hybridization will occur at 30°C in 750 mM NaCl, 75 mM trisodium citrate, and 1% SDS. In a more preferred embodiment, hybridization will occur at 37°C in 500 mM NaCl, 50 mM trisodium citrate, 1% SDS, 35% formamide, and 100 µg/ml denatured salmon sperm DNA (ssDNA). In a

most preferred embodiment, hybridization will occur at 42°C in 250 mM NaCl, 25 mM trisodium citrate, 1% SDS, 50 % formamide, and 200 µg/ml ssDNA. Useful variations on these conditions will be readily apparent to those skilled in the art.

The washing steps which follow hybridization can also vary in stringency. Wash stringency conditions can be defined by salt concentration and by temperature. As above, wash stringency can be increased by decreasing salt concentration or by increasing temperature. For example, stringent salt concentration for the wash steps will preferably be less than about 30 mM NaCl and 3 mM trisodium citrate, and most preferably less than about 15 mM NaCl and 1.5 mM trisodium citrate. Stringent temperature conditions for the wash steps will ordinarily include temperature of at least about 25°C, more preferably of at least about 42°C, and most preferably of at least about 68°C. In a preferred embodiment, wash steps will occur at 25°C in 30 mM NaCl, 3 mM trisodium citrate, and 0.1% SDS. In a more preferred embodiment, wash steps will occur at 42°C in 15 mM NaCl, 1.5 mM trisodium citrate, and 0.1% SDS. In a most preferred embodiment, wash steps will occur at 68°C in 15 mM NaCl, 1.5 mM trisodium citrate, and 0.1% SDS. Additional variations on these conditions will be readily apparent to those skilled in the art.

Methods for DNA sequencing are well known in the art and may be used to practice any of the embodiments of the invention. The methods may employ such enzymes as the Klenow fragment of DNA polymerase I, SEQUENASE (US Biochemical, Cleveland OH), Taq polymerase (Perkin-Elmer), thermostable T7 polymerase (Amersham Pharmacia Biotech, Piscataway NJ), or combinations of polymerases and proofreading exonucleases such as those found in the ELONGASE amplification system (Life Technologies, Gaithersburg MD). Preferably, sequence preparation is automated with machines such as the Hamilton MICROLAB 2200 (Hamilton, Reno NV), Peltier thermal cycler 200 (PTC200; MJ Research, Watertown MA) and the ABI CATALYST 800 (Perkin-Elmer). Sequencing is then carried out using either ABI 373 or 377 DNA sequencing systems (Perkin-Elmer), the MEGABACE 1000 DNA sequencing system (Molecular Dynamics, Sunnyvale CA), or other systems known in the art. The resulting sequences are analyzed using a variety of algorithms which are well known in the art. (See, e.g., Ausubel, F.M. (1997) Short Protocols in Molecular Biology, John Wiley & Sons, New York NY, unit 7.7; Meyers, R.A. (1995) Molecular Biology and Biotechnology, Wiley VCH, New York NY, pp. 856-853.)

The nucleic acid sequences encoding PPRG may be extended utilizing a partial nucleotide sequence and employing various PCR-based methods known in the art to detect upstream sequences, such as promoters and regulatory elements. For example, one method which may be employed, restriction-site PCR, uses universal and nested primers to amplify unknown sequence

from genomic DNA within a cloning vector. (See, e.g., Sarkar, G. (1993) PCR Methods Applic. 2:318-322.) Another method, inverse PCR, uses primers that extend in divergent directions to amplify unknown sequence from a circularized template. The template is derived from restriction fragments comprising a known genomic locus and surrounding sequences. (See, e.g., Triglia, T. et al. (1988) Nucleic Acids Res. 16:8186.) A third method, capture PCR, involves PCR amplification of DNA fragments adjacent to known sequences in human and yeast artificial chromosome DNA. (See, e.g., Lagerstrom, M. et al. (1991) PCR Methods Applic. 1:111-119.) In this method, multiple restriction enzyme digestions and ligations may be used to insert an engineered double-stranded sequence into a region of unknown sequence before performing PCR.

10 Other methods which may be used to retrieve unknown sequences are known in the art. (See, e.g., Parker, J.D. et al. (1991) Nucleic Acids Res. 19:3055-3060). Additionally, one may use PCR, nested primers, and PROMOTERFINDER libraries (Clontech, Palo Alto CA) to walk genomic DNA. This procedure avoids the need to screen libraries and is useful in finding intron/exon junctions. For all PCR-based methods, primers may be designed using commercially available

15 software, such as OLIGO 4.06 Primer Analysis software (National Biosciences, Plymouth MN) or another appropriate program, to be about 22 to 30 nucleotides in length, to have a GC content of about 50% or more, and to anneal to the template at temperatures of about 68°C to 72°C.

When screening for full-length cDNAs, it is preferable to use libraries that have been size-selected to include larger cDNAs. In addition, random-primed libraries, which often include

20 sequences containing the 5' regions of genes, are preferable for situations in which an oligo d(T) library does not yield a full-length cDNA. Genomic libraries may be useful for extension of sequence into 5' non-transcribed regulatory regions.

Capillary electrophoresis systems which are commercially available may be used to analyze the size or confirm the nucleotide sequence of sequencing or PCR products. In particular,

25 capillary sequencing may employ flowable polymers for electrophoretic separation, four different nucleotide-specific, laser-stimulated fluorescent dyes, and a charge coupled device camera for detection of the emitted wavelengths. Output/light intensity may be converted to electrical signal using appropriate software (e.g., GENOTYPER and SEQUENCE NAVIGATOR, Perkin-Elmer), and the entire process from loading of samples to computer analysis and electronic data display

30 may be computer controlled. Capillary electrophoresis is especially preferable for sequencing small DNA fragments which may be present in limited amounts in a particular sample.

In another embodiment of the invention, polynucleotide sequences or fragments thereof which encode PPRG may be cloned in recombinant DNA molecules that direct expression of PPRG, or fragments or functional equivalents thereof, in appropriate host cells. Due to the

inherent degeneracy of the genetic code, other DNA sequences which encode substantially the same or a functionally equivalent amino acid sequence may be produced and used to express PPRG.

The nucleotide sequences of the present invention can be engineered using methods generally known in the art in order to alter PPRG-encoding sequences for a variety of purposes including, but not limited to, modification of the cloning, processing, and/or expression of the gene product. DNA shuffling by random fragmentation and PCR reassembly of gene fragments and synthetic oligonucleotides may be used to engineer the nucleotide sequences. For example, oligonucleotide-mediated site-directed mutagenesis may be used to introduce mutations that create new restriction sites, alter glycosylation patterns, change codon preference, produce splice variants, and so forth.

In another embodiment, sequences encoding PPRG may be synthesized, in whole or in part, using chemical methods well known in the art. (See, e.g., Caruthers, M.H. et al. (1980) *Nucleic Acids Symp. Ser.* 7:215-223; Horn, T. et al. (1980) *Nucleic Acids Symp. Ser.* 7:225-232.) Alternatively, PPRG itself or a fragment thereof may be synthesized using chemical methods. For example, peptide synthesis can be performed using various solid-phase techniques. (See, e.g., Roberge, J.Y. et al. (1995) *Science* 269:202-204.) Automated synthesis may be achieved using the ABI 431A peptide synthesizer (Perkin-Elmer). Additionally, the amino acid sequence of PPRG, or any part thereof, may be altered during direct synthesis and/or combined with sequences from other proteins, or any part thereof, to produce a variant polypeptide.

The peptide may be substantially purified by preparative high performance liquid chromatography. (See, e.g., Chiez, R.M. and F.Z. Regnier (1990) *Methods Enzymol.* 182:392-421.) The composition of the synthetic peptides may be confirmed by amino acid analysis or by sequencing. (See, e.g., Creighton, T. (1984) Proteins, Structures and Molecular Properties, WH Freeman, New York NY.)

In order to express a biologically active PPRG, the nucleotide sequences encoding PPRG or derivatives thereof may be inserted into an appropriate expression vector, i.e., a vector which contains the necessary elements for transcriptional and translational control of the inserted coding sequence in a suitable host. These elements include regulatory sequences, such as enhancers, constitutive and inducible promoters, and 5' and 3' untranslated regions in the vector and in polynucleotide sequences encoding PPRG. Such elements may vary in their strength and specificity. Specific initiation signals may also be used to achieve more efficient translation of sequences encoding PPRG. Such signals include the ATG initiation codon and adjacent sequences, e.g. the Kozak sequence. In cases where sequences encoding PPRG and its initiation

codon and upstream regulatory sequences are inserted into the appropriate expression vector, no additional transcriptional or translational control signals may be needed. However, in cases where only coding sequence, or a fragment thereof, is inserted, exogenous translational control signals including an in-frame ATG initiation codon should be provided by the vector. Exogenous
5 translational elements and initiation codons may be of various origins, both natural and synthetic. The efficiency of expression may be enhanced by the inclusion of enhancers appropriate for the particular host cell system used. (See, e.g., Scharf, D. et al. (1994) *Results Probl. Cell Differ.* 20:125-162.)

Methods which are well known to those skilled in the art may be used to construct
10 expression vectors containing sequences encoding PPRG and appropriate transcriptional and translational control elements. These methods include in vitro recombinant DNA techniques, synthetic techniques, and in vivo genetic recombination. (See, e.g., Sambrook, J. et al. (1989) Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Press, Plainview NY, ch. 4, 8, and 16-17; Ausubel, F.M. et al. (1995) Current Protocols in Molecular Biology, John Wiley & Sons,
15 New York NY, ch. 9, 13, and 16.)

A variety of expression vector/host systems may be utilized to contain and express sequences encoding PPRG. These include, but are not limited to, microorganisms such as bacteria transformed with recombinant bacteriophage, plasmid, or cosmid DNA expression vectors; yeast transformed with yeast expression vectors; insect cell systems infected with viral expression
20 vectors (e.g., baculovirus); plant cell systems transformed with viral expression vectors (e.g., cauliflower mosaic virus, CaMV, or tobacco mosaic virus, TMV) or with bacterial expression vectors (e.g., Ti or pBR322 plasmids); or animal cell systems. The invention is not limited by the host cell employed.

In bacterial systems, a number of cloning and expression vectors may be selected
25 depending upon the use intended for polynucleotide sequences encoding PPRG. For example, routine cloning, subcloning, and propagation of polynucleotide sequences encoding PPRG can be achieved using a multifunctional E. coli vector such as PBLUESCRIPT (Stratagene, La Jolla CA) or pSPORT1 plasmid (Life Technologies). Ligation of sequences encoding PPRG into the vector's multiple cloning site disrupts the *lacZ* gene, allowing a colorimetric screening procedure
30 for identification of transformed bacteria containing recombinant molecules. In addition, these vectors may be useful for in vitro transcription, dideoxy sequencing, single strand rescue with helper phage, and creation of nested deletions in the cloned sequence. (See, e.g., Van Heeke, G. and S.M. Schuster (1989) *J. Biol. Chem.* 264:5503-5509.) When large quantities of PPRG are needed, e.g. for the production of antibodies, vectors which direct high level expression of PPRG

may be used. For example, vectors containing the strong, inducible T5 or T7 bacteriophage promoter may be used.

Yeast expression systems may be used for production of PPRG. A number of vectors containing constitutive or inducible promoters, such as alpha factor, alcohol oxidase, and PGH promoters, may be used in the yeast Saccharomyces cerevisiae or Pichia pastoris. In addition, such vectors direct either the secretion or intracellular retention of expressed proteins and enable integration of foreign sequences into the host genome for stable propagation. (See, e.g., Ausubel, 1995, supra; Grant et al. (1987) *Methods Enzymol.* 153:516-54; and Scorer, C. A. et al. (1994) *Bio/Technology* 12:181-184.)

Plant systems may also be used for expression of PPRG. Transcription of sequences encoding PPRG may be driven viral promoters, e.g., the 35S and 19S promoters of CaMV used alone or in combination with the omega leader sequence from TMV (Takamatsu, N. (1987) *EMBO J.* 6:307-311). Alternatively, plant promoters such as the small subunit of RUBISCO or heat shock promoters may be used. (See, e.g., Coruzzi, G. et al. (1984) *EMBO J.* 3:1671-1680; Broglie, R. et al. (1984) *Science* 224:838-843; and Winter, J. et al. (1991) *Results Probl. Cell Differ.* 17:85-105.) These constructs can be introduced into plant cells by direct DNA transformation or pathogen-mediated transfection. (See, e.g., The McGraw Hill Yearbook of Science and Technology (1992) McGraw Hill, New York NY, pp. 191-196.)

In mammalian cells, a number of viral-based expression systems may be utilized. In cases where an adenovirus is used as an expression vector, sequences encoding PPRG may be ligated into an adenovirus transcription/translation complex consisting of the late promoter and tripartite leader sequence. Insertion in a non-essential E1 or E3 region of the viral genome may be used to obtain infective virus which expresses PPRG in host cells. (See, e.g., Logan, J. and T. Shenk (1984) *Proc. Natl. Acad. Sci. U.S.A.* 81:3655-3659.) In addition, transcription enhancers, such as the Rous sarcoma virus (RSV) enhancer, may be used to increase expression in mammalian host cells. SV40 or EBV-based vectors may also be used for high-level protein expression.

Human artificial chromosomes (HACs) may also be employed to deliver larger fragments of DNA than can be contained in and expressed from a plasmid. HACs of about 6 kb to 10 Mb are constructed and delivered via conventional delivery methods (liposomes, polycationic amino polymers, or vesicles) for therapeutic purposes. (See, e.g., Harrington, J.J. et al. (1997) *Nat. Genet.* 15:345-355.)

For long term production of recombinant proteins in mammalian systems, stable expression of PPRG in cell lines is preferred. For example, sequences encoding PPRG can be transformed into cell lines using expression vectors which may contain viral origins of replication

and/or endogenous expression elements and a selectable marker gene on the same or on a separate vector. Following the introduction of the vector, cells may be allowed to grow for about 1 to 2 days in enriched media before being switched to selective media. The purpose of the selectable marker is to confer resistance to a selective agent, and its presence allows growth and recovery of cells which successfully express the introduced sequences. Resistant clones of stably transformed cells may be propagated using tissue culture techniques appropriate to the cell type.

Any number of selection systems may be used to recover transformed cell lines. These include, but are not limited to, the herpes simplex virus thymidine kinase and adenine phosphoribosyltransferase genes, for use in *tk* or *ap^r* cells, respectively. (See, e.g., Wigler, M. et al. (1977) Cell 11:223-232; Lowy, I. et al. (1980) Cell 22:817-823.) Also, antimetabolite, antibiotic, or herbicide resistance can be used as the basis for selection. For example, *dhfr* confers resistance to methotrexate; *neo* confers resistance to the aminoglycosides neomycin and G-418; and *als* or *pat* confer resistance to chlorsulfuron and phosphinotricin acetyltransferase, respectively. (See, e.g., Wigler, M. et al. (1980) Proc. Natl. Acad. Sci. U.S.A. 77:3567-3570; Colbere-Garapin, F. et al. (1981) J. Mol. Biol. 150:1-14.) Additional selectable genes have been described, e.g., *trpB* and *hisD*, which alter cellular requirements for metabolites. (See, e.g., Hartman, S.C. and R.C. Mulligan (1988) Proc. Natl. Acad. Sci. U.S.A. 85:8047-8051.) Visible markers, e.g., anthocyanins, green fluorescent proteins (GFP; Clontech), β glucuronidase and its substrate β -glucuronide, or luciferase and its substrate luciferin may be used. These markers can be used not only to identify transformants, but also to quantify the amount of transient or stable protein expression attributable to a specific vector system. (See, e.g., Rhodes, C.A. (1995) Methods Mol. Biol. 55:121-131.)

Although the presence/absence of marker gene expression suggests that the gene of interest is also present, the presence and expression of the gene may need to be confirmed. For example, if the sequence encoding PPRG is inserted within a marker gene sequence, transformed cells containing sequences encoding PPRG can be identified by the absence of marker gene function. Alternatively, a marker gene can be placed in tandem with a sequence encoding PPRG under the control of a single promoter. Expression of the marker gene in response to induction or selection usually indicates expression of the tandem gene as well.

In general, host cells that contain the nucleic acid sequence encoding PPRG and that express PPRG may be identified by a variety of procedures known to those of skill in the art. These procedures include, but are not limited to, DNA-DNA or DNA-RNA hybridizations, PCR amplification, and protein bioassay or immunoassay techniques which include membrane, solution, or chip based technologies for the detection and/or quantification of nucleic acid or

protein sequences.

Immunological methods for detecting and measuring the expression of PPRG using either specific polyclonal or monoclonal antibodies are known in the art. Examples of such techniques include enzyme-linked immunosorbent assays (ELISAs), radioimmunoassays (RIAs), and
5 fluorescence activated cell sorting (FACS). A two-site, monoclonal-based immunoassay utilizing monoclonal antibodies reactive to two non-interfering epitopes on PPRG is preferred, but a competitive binding assay may be employed. These and other assays are well known in the art. (See, e.g., Hampton, R. et al. (1990) Serological Methods, a Laboratory Manual, APS Press, St. Paul MN, Sect. IV; Coligan, J.E. et al. (1997) Current Protocols in Immunology, Greene Pub.
10 Associates and Wiley-Interscience, New York NY; and Pound, J.D. (1998) Immunochemical Protocols, Humana Press, Totowa NJ).

A wide variety of labels and conjugation techniques are known by those skilled in the art and may be used in various nucleic acid and amino acid assays. Means for producing labeled hybridization or PCR probes for detecting sequences related to polynucleotides encoding PPRG
15 include oligolabeling, nick translation, end-labeling, or PCR amplification using a labeled nucleotide. Alternatively, the sequences encoding PPRG, or any fragments thereof, may be cloned into a vector for the production of an mRNA probe. Such vectors are known in the art, are commercially available, and may be used to synthesize RNA probes in vitro by addition of an appropriate RNA polymerase such as T7, T3, or SP6 and labeled nucleotides. These procedures
20 may be conducted using a variety of commercially available kits, such as those provided by Amersham Pharmacia Biotech, Promega (Madison WI), and US Biochemical. Suitable reporter molecules or labels which may be used for ease of detection include radionuclides, enzymes, fluorescent, chemiluminescent, or chromogenic agents, as well as substrates, cofactors, inhibitors, magnetic particles, and the like.

25 Host cells transformed with nucleotide sequences encoding PPRG may be cultured under conditions suitable for the expression and recovery of the protein from cell culture. The protein produced by a transformed cell may be secreted or retained intracellularly depending on the sequence and/or the vector used. As will be understood by those of skill in the art, expression vectors containing polynucleotides which encode PPRG may be designed to contain signal
30 sequences which direct secretion of PPRG through a prokaryotic or eukaryotic cell membrane.

In addition, a host cell strain may be chosen for its ability to modulate expression of the inserted sequences or to process the expressed protein in the desired fashion. Such modifications of the polypeptide include, but are not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation, and acylation. Post-translational processing which cleaves a "prepro"

form of the protein may also be used to specify protein targeting, folding, and/or activity.

Different host cells which have specific cellular machinery and characteristic mechanisms for post-translational activities (e.g., CHO, HeLa, MDCK, HEK293, and WI38), are available from the American Type Culture Collection (ATCC, Bethesda MD) and may be chosen to ensure the

5 correct modification and processing of the foreign protein.

In another embodiment of the invention, natural, modified, or recombinant nucleic acid sequences encoding PPRG may be ligated to a heterologous sequence resulting in translation of a fusion protein in any of the aforementioned host systems. For example, a chimeric PPRG protein containing a heterologous moiety that can be recognized by a commercially available antibody
10 may facilitate the screening of peptide libraries for inhibitors of PPRG activity. Heterologous protein and peptide moieties may also facilitate purification of fusion proteins using commercially available affinity matrices. Such moieties include, but are not limited to, glutathione S-transferase (GST), maltose binding protein (MBP), thioredoxin (Trx), calmodulin binding peptide (CBP), 6-His, FLAG, *c-myc*, and hemagglutinin (HA). GST, MBP, Trx, CBP, and 6-His enable purification
15 of their cognate fusion proteins on immobilized glutathione, maltose, phenylarsine oxide, calmodulin, and metal-chelate resins, respectively. FLAG, *c-myc*, and hemagglutinin (HA) enable immunoaffinity purification of fusion proteins using commercially available monoclonal and polyclonal antibodies that specifically recognize these epitope tags. A fusion protein may also be engineered to contain a proteolytic cleavage site located between the PPRG encoding sequence
20 and the heterologous protein sequence, so that PPRG may be cleaved away from the heterologous moiety following purification. Methods for fusion protein expression and purification are discussed in Ausubel (1995, supra, ch 10). A variety of commercially available kits may also be used to facilitate expression and purification of fusion proteins.

In a further embodiment of the invention, synthesis of radiolabeled PPRG may be
25 achieved in vitro using the TNT rabbit reticulocyte lysate or wheat germ extract systems (Promega). These systems couple transcription and translation of protein-coding sequences operably associated with the T7, T3, or SP6 promoters. Translation takes place in the presence of a radiolabeled amino acid precursor, preferably ³⁵S-methionine.

Fragments of PPRG may be produced not only by recombinant production, but also by
30 direct peptide synthesis using solid-phase techniques. (See, e.g., Creighton, supra, pp. 55-60.) Protein synthesis may be performed by manual techniques or by automation. Automated synthesis may be achieved, for example, using the ABI 431A peptide synthesizer (Perkin-Elmer). Various fragments of PPRG may be synthesized separately and then combined to produce the full length molecule.

THERAPEUTICS

Chemical and structural similarity, e.g., in the context of sequences and motifs, exists between regions of PPRG and proteases and associated proteins. In addition, the expression of PPRG is closely associated with cell proliferative conditions, including cancer, and with inflammation and the immune response. Therefore, PPRG appears to play a role in cell proliferative and immune disorders. In the treatment of cell proliferative and immune disorders associated with increased PPRG expression or activity, it is desirable to decrease the expression or activity of PPRG. In the treatment of the above conditions associated with decreased PPRG expression or activity, it is desirable to increase the expression or activity of PPRG.

Therefore, in one embodiment, PPRG or a fragment or derivative thereof may be administered to a subject to treat or prevent a disorder associated with decreased expression or activity of PPRG. Examples of such disorders include, but are not limited to, a cell proliferative disorder such as actinic keratosis, arteriosclerosis, atherosclerosis, bursitis, cirrhosis, hepatitis, mixed connective tissue disease (MCTD), myelofibrosis, paroxysmal nocturnal hemoglobinuria, polycythemia vera, psoriasis, primary thrombocythemia, and cancers including adenocarcinoma, leukemia, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, and, in particular, cancers of the adrenal gland, bladder, bone, bone marrow, brain, breast, cervix, gall bladder, ganglia, gastrointestinal tract, heart, kidney, liver, lung, muscle, ovary, pancreas, parathyroid, penis, prostate, salivary glands, skin, spleen, testis, thymus, thyroid, and uterus; and an immune disorder such as acquired immunodeficiency syndrome (AIDS), Addison's disease, adult respiratory distress syndrome, allergies, ankylosing spondylitis, amyloidosis, anemia, asthma, atherosclerosis, autoimmune hemolytic anemia, autoimmune thyroiditis, autoimmune polyendocrinopathy-candidiasis-ectodermal dystrophy (APECED), bronchitis, cholecystitis, contact dermatitis, Crohn's disease, atopic dermatitis, dermatomyositis, diabetes mellitus, emphysema, episodic lymphopenia with lymphocytotoxins, erythroblastosis fetalis, erythema nodosum, atrophic gastritis, glomerulonephritis, Goodpasture's syndrome, gout, Graves' disease, Hashimoto's thyroiditis, hypereosinophilia, irritable bowel syndrome, multiple sclerosis, myasthenia gravis, myocardial or pericardial inflammation, osteoarthritis, osteoporosis, pancreatitis, polymyositis, psoriasis, Reiter's syndrome, rheumatoid arthritis, scleroderma, Sjögren's syndrome, systemic anaphylaxis, systemic lupus erythematosus, systemic sclerosis, thrombocytopenic purpura, ulcerative colitis, uveitis, Werner syndrome, complications of cancer, hemodialysis, and extracorporeal circulation, viral, bacterial, fungal, parasitic, protozoal, and helminthic infections, and trauma.

In another embodiment, a vector capable of expressing PPRG or a fragment or derivative thereof may be administered to a subject to treat or prevent a disorder associated with decreased

expression or activity of PPRG including, but not limited to, those described above.

In a further embodiment, a pharmaceutical composition comprising a substantially purified PPRG in conjunction with a suitable pharmaceutical carrier may be administered to a subject to treat or prevent a disorder associated with decreased expression or activity of PPRG including, but not limited to, those provided above.

In still another embodiment, an agonist which modulates the activity of PPRG may be administered to a subject to treat or prevent a disorder associated with decreased expression or activity of PPRG including, but not limited to, those listed above.

In a further embodiment, an antagonist of PPRG may be administered to a subject to treat or prevent a disorder associated with increased expression or activity of PPRG. Examples of such disorders include, but are not limited to, those described above. In one aspect, an antibody which specifically binds PPRG may be used directly as an antagonist or indirectly as a targeting or delivery mechanism for bringing a pharmaceutical agent to cells or tissue which express PPRG.

In an additional embodiment, a vector expressing the complement of the polynucleotide encoding PPRG may be administered to a subject to treat or prevent a disorder associated with increased expression or activity of PPRG including, but not limited to, those described above.

In other embodiments, any of the proteins, antagonists, antibodies, agonists, complementary sequences, or vectors of the invention may be administered in combination with other appropriate therapeutic agents. Selection of the appropriate agents for use in combination therapy may be made by one of ordinary skill in the art, according to conventional pharmaceutical principles. The combination of therapeutic agents may act synergistically to effect the treatment or prevention of the various disorders described above. Using this approach, one may be able to achieve therapeutic efficacy with lower dosages of each agent, thus reducing the potential for adverse side effects.

An antagonist of PPRG may be produced using methods which are generally known in the art. In particular, purified PPRG may be used to produce antibodies or to screen libraries of pharmaceutical agents to identify those which specifically bind PPRG. Antibodies to PPRG may also be generated using methods that are well known in the art. Such antibodies may include, but are not limited to, polyclonal, monoclonal, chimeric, and single chain antibodies, Fab fragments, and fragments produced by a Fab expression library. Neutralizing antibodies (i.e., those which inhibit dimer formation) are especially preferred for therapeutic use.

For the production of antibodies, various hosts including goats, rabbits, rats, mice, humans, and others may be immunized by injection with PPRG or with any fragment or oligopeptide thereof which has immunogenic properties. Depending on the host species, various

adjuvants may be used to increase immunological response. Such adjuvants include, but are not limited to, Freund's, mineral gels such as aluminum hydroxide, and surface active substances such as lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, KLH, and dinitrophenol. Among adjuvants used in humans, BCG (bacilli Calmette-Guerin) and Corynebacterium parvum are especially preferable.

It is preferred that the oligopeptides, peptides, or fragments used to induce antibodies to PPRG have an amino acid sequence consisting of at least about 5 amino acids, and, more preferably, of at least about 10 amino acids. It is also preferable that these oligopeptides, peptides, or fragments are identical to a portion of the amino acid sequence of the natural protein and contain the entire amino acid sequence of a small, naturally occurring molecule. Short stretches of PPRG amino acids may be fused with those of another protein, such as KLH, and antibodies to the chimeric molecule may be produced.

Monoclonal antibodies to PPRG may be prepared using any technique which provides for the production of antibody molecules by continuous cell lines in culture. These include, but are not limited to, the hybridoma technique, the human B-cell hybridoma technique, and the EBV-hybridoma technique. (See, e.g., Kohler, G. et al. (1975) Nature 256:495-497; Kozbor, D. et al. (1985) J. Immunol. Methods 81:31-42; Cote, R.J. et al. (1983) Proc. Natl. Acad. Sci. U.S.A. 80:2026-2030; and Cole, S.P. et al. (1984) Mol. Cell Biol. 62:109-120.)

In addition, techniques developed for the production of "chimeric antibodies," such as the splicing of mouse antibody genes to human antibody genes to obtain a molecule with appropriate antigen specificity and biological activity, can be used. (See, e.g., Morrison, S.L. et al. (1984) Proc. Natl. Acad. Sci. U.S.A. 81:6851-6855; Neuberger, M.S. et al. (1984) Nature 312:604-608; and Takeda, S. et al. (1985) Nature 314:452-454.) Alternatively, techniques described for the production of single chain antibodies may be adapted, using methods known in the art, to produce PPRG-specific single chain antibodies. Antibodies with related specificity, but of distinct idiotypic composition, may be generated by chain shuffling from random combinatorial immunoglobulin libraries. (See, e.g., Burton D.R. (1991) Proc. Natl. Acad. Sci. U.S.A. 88:10134-10137.)

Antibodies may also be produced by inducing in vivo production in the lymphocyte population or by screening immunoglobulin libraries or panels of highly specific binding reagents as disclosed in the literature. (See, e.g., Orlandi, R. et al. (1989) Proc. Natl. Acad. Sci. U.S.A. 86:3833-3837; Winter, G. et al. (1991) Nature 349:293-299.)

Antibody fragments which contain specific binding sites for PPRG may also be generated. For example, such fragments include, but are not limited to, F(ab')₂ fragments produced by

pepsin digestion of the antibody molecule and Fab fragments generated by reducing the disulfide bridges of the F(ab')₂ fragments. Alternatively, Fab expression libraries may be constructed to allow rapid and easy identification of monoclonal Fab fragments with the desired specificity. (See, e.g., Huse, W.D. et al. (1989) Science 246:1275-1281.)

5 Various immunoassays may be used for screening to identify antibodies having the desired specificity. Numerous protocols for competitive binding or immunoradiometric assays using either polyclonal or monoclonal antibodies with established specificities are well known in the art. Such immunoassays typically involve the measurement of complex formation between PPRG and its specific antibody. A two-site, monoclonal-based immunoassay utilizing monoclonal
10 antibodies reactive to two non-interfering PPRG epitopes is preferred, but a competitive binding assay may also be employed (Pound, supra).

Various methods such as Scatchard analysis in conjunction with radioimmunoassay techniques may be used to assess the affinity of antibodies for PPRG. Affinity is expressed as an association constant, K_a , which is defined as the molar concentration of PPRG-antibody complex
15 divided by the molar concentrations of free antigen and free antibody under equilibrium conditions. The K_a determined for a preparation of polyclonal antibodies, which are heterogeneous in their affinities for multiple PPRG epitopes, represents the average affinity, or avidity, of the antibodies for PPRG. The K_a determined for a preparation of monoclonal antibodies, which are monospecific for a particular PPRG epitope, represents a true measure of
20 affinity. High-affinity antibody preparations with K_a ranging from about 10^9 to 10^{12} L/mole are preferred for use in immunoassays in which the PPRG-antibody complex must withstand rigorous manipulations. Low-affinity antibody preparations with K_a ranging from about 10^6 to 10^7 L/mole are preferred for use in immunopurification and similar procedures which ultimately require dissociation of PPRG, preferably in active form, from the antibody (Catty, D. (1988) Antibodies,
25 Volume I: A Practical Approach, IRL Press, Washington, DC; Liddell, J.E. and Cryer, A. (1991) A Practical Guide to Monoclonal Antibodies, John Wiley & Sons, New York NY).

The titer and avidity of polyclonal antibody preparations may be further evaluated to determine the quality and suitability of such preparations for certain downstream applications. For example, a polyclonal antibody preparation containing at least 1-2 mg specific antibody/ml,
30 preferably 5-10 mg specific antibody/ml, is preferred for use in procedures requiring precipitation of PPRG-antibody complexes. Procedures for evaluating antibody specificity, titer, and avidity, and guidelines for antibody quality and usage in various applications, are generally available. (See, e.g., Catty, supra, and Coligan et al. supra.)

In another embodiment of the invention, the polynucleotides encoding PPRG, or any

fragment or complement thereof, may be used for therapeutic purposes. In one aspect, the complement of the polynucleotide encoding PPRG may be used in situations in which it would be desirable to block the transcription of the mRNA. In particular, cells may be transformed with sequences complementary to polynucleotides encoding PPRG. Thus, complementary molecules
5 or fragments may be used to modulate PPRG activity, or to achieve regulation of gene function. Such technology is now well known in the art, and sense or antisense oligonucleotides or larger fragments can be designed from various locations along the coding or control regions of sequences encoding PPRG.

Expression vectors derived from retroviruses, adenoviruses, or herpes or vaccinia viruses,
10 or from various bacterial plasmids, may be used for delivery of nucleotide sequences to the targeted organ, tissue, or cell population. Methods which are well known to those skilled in the art can be used to construct vectors to express nucleic acid sequences complementary to the polynucleotides encoding PPRG. (See, e.g., Sambrook, supra; Ausubel, 1995, supra.)

Genes encoding PPRG can be turned off by transforming a cell or tissue with expression
15 vectors which express high levels of a polynucleotide, or fragment thereof, encoding PPRG. Such constructs may be used to introduce untranslatable sense or antisense sequences into a cell. Even in the absence of integration into the DNA, such vectors may continue to transcribe RNA molecules until they are disabled by endogenous nucleases. Transient expression may last for a month or more with a non-replicating vector, and may last even longer if appropriate replication
20 elements are part of the vector system.

As mentioned above, modifications of gene expression can be obtained by designing complementary sequences or antisense molecules (DNA, RNA, or PNA) to the control, 5', or regulatory regions of the gene encoding PPRG. Oligonucleotides derived from the transcription initiation site, e.g., between about positions -10 and +10 from the start site, are preferred.
25 Similarly, inhibition can be achieved using triple helix base-pairing methodology. Triple helix pairing is useful because it causes inhibition of the ability of the double helix to open sufficiently for the binding of polymerases, transcription factors, or regulatory molecules. Recent therapeutic advances using triplex DNA have been described in the literature. (See, e.g., Gee, J.E. et al. (1994) in Huber, B.E. and B.I. Carr, Molecular and Immunologic Approaches, Futura Publishing,
30 Mt. Kisco NY, pp. 163-177.) A complementary sequence or antisense molecule may also be designed to block translation of mRNA by preventing the transcript from binding to ribosomes.

Ribozymes, enzymatic RNA molecules, may also be used to catalyze the specific cleavage of RNA. The mechanism of ribozyme action involves sequence-specific hybridization of the ribozyme molecule to complementary target RNA, followed by endonucleolytic cleavage. For

example, engineered hammerhead motif ribozyme molecules may specifically and efficiently catalyze endonucleolytic cleavage of sequences encoding PPRG.

Specific ribozyme cleavage sites within any potential RNA target are initially identified by scanning the target molecule for ribozyme cleavage sites, including the following sequences:

- 5 GUA, GUU, and GUC. Once identified, short RNA sequences of between 15 and 20 ribonucleotides, corresponding to the region of the target gene containing the cleavage site, may be evaluated for secondary structural features which may render the oligonucleotide inoperable. The suitability of candidate targets may also be evaluated by testing accessibility to hybridization with complementary oligonucleotides using ribonuclease protection assays.
- 10 Complementary ribonucleic acid molecules and ribozymes of the invention may be prepared by any method known in the art for the synthesis of nucleic acid molecules. These include techniques for chemically synthesizing oligonucleotides such as solid phase phosphoramidite chemical synthesis. Alternatively, RNA molecules may be generated by in vitro and in vivo transcription of DNA sequences encoding PPRG. Such DNA sequences may be
- 15 incorporated into a wide variety of vectors with suitable RNA polymerase promoters such as T7 or SP6. Alternatively, these cDNA constructs that synthesize complementary RNA, constitutively or inducibly, can be introduced into cell lines, cells, or tissues.

RNA molecules may be modified to increase intracellular stability and half-life. Possible modifications include, but are not limited to, the addition of flanking sequences at the 5' and/or 3' ends of the molecule, or the use of phosphorothioate or 2' O-methyl rather than phosphodiesterase linkages within the backbone of the molecule. This concept is inherent in the production of PNAs and can be extended in all of these molecules by the inclusion of nontraditional bases such as inosine, queosine, and wybutosine, as well as acetyl-, methyl-, thio-, and similarly modified forms of adenine, cytidine, guanine, thymine, and uridine which are not as easily recognized by

20 endogenous endonucleases.

Many methods for introducing vectors into cells or tissues are available and equally suitable for use in vivo, in vitro, and ex vivo. For ex vivo therapy, vectors may be introduced into stem cells taken from the patient and clonally propagated for autologous transplant back into that same patient. Delivery by transfection, by liposome injections, or by polycationic amino polymers

30 may be achieved using methods which are well known in the art. (See, e.g., Goldman, C.K. et al. (1997) Nat. Biotech. 15:462-466.)

Any of the therapeutic methods described above may be applied to any subject in need of such therapy, including, for example, mammals such as dogs, cats, cows, horses, rabbits, monkeys, and most preferably, humans.

An additional embodiment of the invention relates to the administration of a pharmaceutical or sterile composition, in conjunction with a pharmaceutically acceptable carrier, for any of the therapeutic effects discussed above. Such pharmaceutical compositions may consist of PPRG, antibodies to PPRG, and mimetics, agonists, antagonists, or inhibitors of PPRG. The compositions may be administered alone or in combination with at least one other agent, such as a stabilizing compound, which may be administered in any sterile, biocompatible pharmaceutical carrier including, but not limited to, saline, buffered saline, dextrose, and water. The compositions may be administered to a patient alone, or in combination with other agents, drugs, or hormones.

The pharmaceutical compositions utilized in this invention may be administered by any number of routes including, but not limited to, oral, intravenous, intramuscular, intra-arterial, intramedullary, intrathecal, intraventricular, transdermal, subcutaneous, intraperitoneal, intranasal, enteral, topical, sublingual, or rectal means.

In addition to the active ingredients, these pharmaceutical compositions may contain suitable pharmaceutically-acceptable carriers comprising excipients and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically. Further details on techniques for formulation and administration may be found in the latest edition of Remington's Pharmaceutical Sciences (Maack Publishing, Easton PA).

Pharmaceutical compositions for oral administration can be formulated using pharmaceutically acceptable carriers well known in the art in dosages suitable for oral administration. Such carriers enable the pharmaceutical compositions to be formulated as tablets, pills, dragees, capsules, liquids, gels, syrups, slurries, suspensions, and the like, for ingestion by the patient.

Pharmaceutical preparations for oral use can be obtained through combining active compounds with solid excipient and processing the resultant mixture of granules (optionally, after grinding) to obtain tablets or dragee cores. Suitable auxiliaries can be added, if desired. Suitable excipients include carbohydrate or protein fillers, such as sugars, including lactose, sucrose, mannitol, and sorbitol; starch from corn, wheat, rice, potato, or other plants; cellulose, such as methyl cellulose, hydroxypropylmethyl-cellulose, or sodium carboxymethylcellulose; gums, including arabic and tragacanth; and proteins, such as gelatin and collagen. If desired, disintegrating or solubilizing agents may be added, such as the cross-linked polyvinyl pyrrolidone, agar, and alginic acid or a salt thereof, such as sodium alginate.

Dragee cores may be used in conjunction with suitable coatings, such as concentrated sugar solutions, which may also contain gum arabic, talc, polyvinylpyrrolidone, carbopol gel, polyethylene glycol, and/or titanium dioxide, lacquer solutions, and suitable organic solvents or

solvent mixtures. Dyestuffs or pigments may be added to the tablets or dragee coatings for product identification or to characterize the quantity of active compound, i.e., dosage.

Pharmaceutical preparations which can be used orally include push-fit capsules made of gelatin, as well as soft, sealed capsules made of gelatin and a coating, such as glycerol or sorbitol.

- 5 Push-fit capsules can contain active ingredients mixed with fillers or binders, such as lactose or starches, lubricants, such as talc or magnesium stearate, and, optionally, stabilizers. In soft capsules, the active compounds may be dissolved or suspended in suitable liquids, such as fatty oils, liquid, or liquid polyethylene glycol with or without stabilizers.

- Pharmaceutical formulations suitable for parenteral administration may be formulated in aqueous solutions, preferably in physiologically compatible buffers such as Hanks' solution, Ringer's solution, or physiologically buffered saline. Aqueous injection suspensions may contain substances which increase the viscosity of the suspension, such as sodium carboxymethyl cellulose, sorbitol, or dextran. Additionally, suspensions of the active compounds may be prepared as appropriate oily injection suspensions. Suitable lipophilic solvents or vehicles include
- 15 fatty oils, such as sesame oil, or synthetic fatty acid esters, such as ethyl oleate, triglycerides, or liposomes. Non-lipid polycationic amino polymers may also be used for delivery. Optionally, the suspension may also contain suitable stabilizers or agents to increase the solubility of the compounds and allow for the preparation of highly concentrated solutions.

- For topical or nasal administration, penetrants appropriate to the particular barrier to be permeated are used in the formulation. Such penetrants are generally known in the art.
- 20

The pharmaceutical compositions of the present invention may be manufactured in a manner that is known in the art, e.g., by means of conventional mixing, dissolving, granulating, dragee-making, levigating, emulsifying, encapsulating, entrapping, or lyophilizing processes.

- The pharmaceutical composition may be provided as a salt and can be formed with many acids, including but not limited to, hydrochloric, sulfuric, acetic, lactic, tartaric, malic, and succinic acids. Salts tend to be more soluble in aqueous or other protonic solvents than are the corresponding free base forms. In other cases, the preferred preparation may be a lyophilized powder which may contain any or all of the following: 1 mM to 50 mM histidine, 0.1% to 2% sucrose, and 2% to 7% mannitol, at a pH range of 4.5 to 5.5, that is combined with buffer prior to
- 25
- 30 use.

After pharmaceutical compositions have been prepared, they can be placed in an appropriate container and labeled for treatment of an indicated condition. For administration of PPRG, such labeling would include amount, frequency, and method of administration.

Pharmaceutical compositions suitable for use in the invention include compositions

wherein the active ingredients are contained in an effective amount to achieve the intended purpose. The determination of an effective dose is well within the capability of those skilled in the art.

For any compound, the therapeutically effective dose can be estimated initially either in
5 cell culture assays, e.g., of neoplastic cells or in animal models such as mice, rats, rabbits, dogs, or pigs. An animal model may also be used to determine the appropriate concentration range and route of administration. Such information can then be used to determine useful doses and routes for administration in humans.

A therapeutically effective dose refers to that amount of active ingredient, for example
10 PPRG or fragments thereof, antibodies of PPRG, and agonists, antagonists or inhibitors of PPRG, which ameliorates the symptoms or condition. Therapeutic efficacy and toxicity may be determined by standard pharmaceutical procedures in cell cultures or with experimental animals, such as by calculating the ED_{50} (the dose therapeutically effective in 50% of the population) or LD_{50} (the dose lethal to 50% of the population) statistics. The dose ratio of toxic to therapeutic
15 effects is the therapeutic index, which can be expressed as the LD_{50}/ED_{50} ratio. Pharmaceutical compositions which exhibit large therapeutic indices are preferred. The data obtained from cell culture assays and animal studies are used to formulate a range of dosage for human use. The dosage contained in such compositions is preferably within a range of circulating concentrations that includes the ED_{50} with little or no toxicity. The dosage varies within this range depending
20 upon the dosage form employed, the sensitivity of the patient, and the route of administration.

The exact dosage will be determined by the practitioner, in light of factors related to the subject requiring treatment. Dosage and administration are adjusted to provide sufficient levels of the active moiety or to maintain the desired effect. Factors which may be taken into account include the severity of the disease state, the general health of the subject, the age, weight, and
25 gender of the subject, time and frequency of administration, drug combination(s), reaction sensitivities, and response to therapy. Long-acting pharmaceutical compositions may be administered every 3 to 4 days, every week, or biweekly depending on the half-life and clearance rate of the particular formulation.

Normal dosage amounts may vary from about 0.1 μg to 100,000 μg , up to a total dose of
30 about 1 gram, depending upon the route of administration. Guidance as to particular dosages and methods of delivery is provided in the literature and generally available to practitioners in the art. Those skilled in the art will employ different formulations for nucleotides than for proteins or their inhibitors. Similarly, delivery of polynucleotides or polypeptides will be specific to particular cells, conditions, locations, etc.

DIAGNOSTICS

In another embodiment, antibodies which specifically bind PPRG may be used for the diagnosis of disorders characterized by expression of PPRG, or in assays to monitor patients being treated with PPRG or agonists, antagonists, or inhibitors of PPRG. Antibodies useful for
5 diagnostic purposes may be prepared in the same manner as described above for therapeutics. Diagnostic assays for PPRG include methods which utilize the antibody and a label to detect PPRG in human body fluids or in extracts of cells or tissues. The antibodies may be used with or without modification, and may be labeled by covalent or non-covalent attachment of a reporter molecule. A wide variety of reporter molecules, several of which are described above, are known
10 in the art and may be used.

A variety of protocols for measuring PPRG, including ELISAs, RIAs, and FACS, are known in the art and provide a basis for diagnosing altered or abnormal levels of PPRG expression. Normal or standard values for PPRG expression are established by combining body fluids or cell extracts taken from normal mammalian subjects, preferably human, with antibody to
15 PPRG under conditions suitable for complex formation. The amount of standard complex formation may be quantitated by various methods, preferably by photometric means. Quantities of PPRG expressed in subject, control, and disease samples from biopsied tissues are compared with the standard values. Deviation between standard and subject values establishes the parameters for diagnosing disease.

In another embodiment of the invention, the polynucleotides encoding PPRG may be used for diagnostic purposes. The polynucleotides which may be used include oligonucleotide sequences, complementary RNA and DNA molecules, and PNAs. The polynucleotides may be used to detect and quantitate gene expression in biopsied tissues in which expression of PPRG may be correlated with disease. The diagnostic assay may be used to determine absence,
20 presence, and excess expression of PPRG, and to monitor regulation of PPRG levels during therapeutic intervention.

In one aspect, hybridization with PCR probes which are capable of detecting polynucleotide sequences, including genomic sequences, encoding PPRG or closely related molecules may be used to identify nucleic acid sequences which encode PPRG. The specificity of
30 the probe, whether it is made from a highly specific region, e.g., the 5' regulatory region, or from a less specific region, e.g., a conserved motif, and the stringency of the hybridization or amplification (maximal, high, intermediate, or low), will determine whether the probe identifies only naturally occurring sequences encoding PPRG, allelic variants, or related sequences.

Probes may also be used for the detection of related sequences, and should preferably

have at least 50% sequence identity to any of the PPRG encoding sequences. The hybridization probes of the subject invention may be DNA or RNA and may be derived from the sequence of SEQ ID NO:21-40 or from genomic sequences including promoters, enhancers, and introns of the PPRG gene.

- 5 Means for producing specific hybridization probes for DNAs encoding PPRG include the cloning of polynucleotide sequences encoding PPRG or PPRG derivatives into vectors for the production of mRNA probes. Such vectors are known in the art, are commercially available, and may be used to synthesize RNA probes in vitro by means of the addition of the appropriate RNA polymerases and the appropriate labeled nucleotides. Hybridization probes may be labeled by a
 10 variety of reporter groups, for example, by radionuclides such as ^{32}P or ^{35}S , or by enzymatic labels, such as alkaline phosphatase coupled to the probe via avidin/biotin coupling systems, and the like.

- Polynucleotide sequences encoding PPRG may be used for the diagnosis of disorders associated with expression of PPRG. Examples of such disorders include, but are not limited to, a cell proliferative disorder such as actinic keratosis, arteriosclerosis, atherosclerosis, bursitis,
 15 cirrhosis, hepatitis, mixed connective tissue disease (MCTD), myelofibrosis, paroxysmal nocturnal hemoglobinuria, polycythemia vera, psoriasis, primary thrombocythemia, and cancers including adenocarcinoma, leukemia, lymphoma, melanoma, myeloma, sarcoma, teratocarcinoma, and, in particular, cancers of the adrenal gland, bladder, bone, bone marrow, brain, breast, cervix, gall bladder, ganglia, gastrointestinal tract, heart, kidney, liver, lung, muscle, ovary, pancreas,
 20 parathyroid, penis, prostate, salivary glands, skin, spleen, testis, thymus, thyroid, and uterus; and an immune disorder such as acquired immunodeficiency syndrome (AIDS), Addison's disease, adult respiratory distress syndrome, allergies, ankylosing spondylitis, amyloidosis, anemia, asthma, atherosclerosis, autoimmune hemolytic anemia, autoimmune thyroiditis, autoimmune polyendocrinopathy-candidiasis-ectodermal dystrophy (APECED), bronchitis, cholecystitis,
 25 contact dermatitis, Crohn's disease, atopic dermatitis, dermatomyositis, diabetes mellitus, emphysema, episodic lymphopenia with lymphocytotoxins, erythroblastosis fetalis, erythema nodosum, atrophic gastritis, glomerulonephritis, Goodpasture's syndrome, gout, Graves' disease, Hashimoto's thyroiditis, hypereosinophilia, irritable bowel syndrome, multiple sclerosis, myasthenia gravis, myocardial or pericardial inflammation, osteoarthritis, osteoporosis,
 30 pancreatitis, polymyositis, psoriasis, Reiter's syndrome, rheumatoid arthritis, scleroderma, Sjögren's syndrome, systemic anaphylaxis, systemic lupus erythematosus, systemic sclerosis, thrombocytopenic purpura, ulcerative colitis, uveitis, Werner syndrome, complications of cancer, hemodialysis, and extracorporeal circulation, viral, bacterial, fungal, parasitic, protozoal, and helminthic infections, and trauma. The polynucleotide sequences encoding PPRG may be used in

Southern or northern analysis, dot blot, or other membrane-based technologies; in PCR technologies; in dipstick, pin, and multiformat ELISA-like assays; and in microarrays utilizing fluids or tissues from patients to detect altered PPRG expression. Such qualitative or quantitative methods are well known in the art.

5 In a particular aspect, the nucleotide sequences encoding PPRG may be useful in assays that detect the presence of associated disorders, particularly those mentioned above. The nucleotide sequences encoding PPRG may be labeled by standard methods and added to a fluid or tissue sample from a patient under conditions suitable for the formation of hybridization complexes. After a suitable incubation period, the sample is washed and the signal is quantitated
10 and compared with a standard value. If the amount of signal in the patient sample is significantly altered in comparison to a control sample then the presence of altered levels of nucleotide sequences encoding PPRG in the sample indicates the presence of the associated disorder. Such assays may also be used to evaluate the efficacy of a particular therapeutic treatment regimen in animal studies, in clinical trials, or to monitor the treatment of an individual patient.

15 In order to provide a basis for the diagnosis of a disorder associated with expression of PPRG, a normal or standard profile for expression is established. This may be accomplished by combining body fluids or cell extracts taken from normal subjects, either animal or human, with a sequence, or a fragment thereof, encoding PPRG, under conditions suitable for hybridization or amplification. Standard hybridization may be quantified by comparing the values obtained from
20 normal subjects with values from an experiment in which a known amount of a substantially purified polynucleotide is used. Standard values obtained in this manner may be compared with values obtained from samples from patients who are symptomatic for a disorder. Deviation from standard values is used to establish the presence of a disorder.

 Once the presence of a disorder is established and a treatment protocol is initiated,
25 hybridization assays may be repeated on a regular basis to determine if the level of expression in the patient begins to approximate that which is observed in the normal subject. The results obtained from successive assays may be used to show the efficacy of treatment over a period ranging from several days to months.

 With respect to cancer, the presence of an abnormal amount of transcript (either under- or
30 overexpressed) in biopsied tissue from an individual may indicate a predisposition for the development of the disease, or may provide a means for detecting the disease prior to the appearance of actual clinical symptoms. A more definitive diagnosis of this type may allow health professionals to employ preventative measures or aggressive treatment earlier thereby preventing the development or further progression of the cancer.

Additional diagnostic uses for oligonucleotides designed from the sequences encoding PPRG may involve the use of PCR. These oligomers may be chemically synthesized, generated enzymatically, or produced in vitro. Oligomers will preferably contain a fragment of a polynucleotide encoding PPRG, or a fragment of a polynucleotide complementary to the
5 polynucleotide encoding PPRG, and will be employed under optimized conditions for identification of a specific gene or condition. Oligomers may also be employed under less stringent conditions for detection or quantitation of closely related DNA or RNA sequences.

Methods which may also be used to quantify the expression of PPRG include radiolabeling or biotinylating nucleotides, coamplification of a control nucleic acid, and
10 interpolating results from standard curves. (See, e.g., Melby, P.C. et al. (1993) *J. Immunol. Methods* 159:235-244; Duplaa, C. et al. (1993) *Anal. Biochem.* 212:229-236.) The speed of quantitation of multiple samples may be accelerated by running the assay in an ELISA format where the oligomer of interest is presented in various dilutions and a spectrophotometric or colorimetric response gives rapid quantitation.

15 In further embodiments, oligonucleotides or longer fragments derived from any of the polynucleotide sequences described herein may be used as targets in a microarray. The microarray can be used to monitor the expression level of large numbers of genes simultaneously and to identify genetic variants, mutations, and polymorphisms. This information may be used to determine gene function, to understand the genetic basis of a disorder, to diagnose a disorder, and
20 to develop and monitor the activities of therapeutic agents.

Microarrays may be prepared, used, and analyzed using methods known in the art. (See, e.g., Brennan, T.M. et al. (1995) U.S. Patent No. 5,474,796; Schena, M. et al. (1996) *Proc. Natl. Acad. Sci. U.S.A.* 93:10614-10619; Baldeschweiler et al. (1995) PCT application WO95/251116; Shalon, D. et al. (1995) PCT application WO95/35505; Heller, R.A. et al. (1997) *Proc. Natl. Acad. Sci. U.S.A.* 94:2150-2155; and Heller, M.J. et al. (1997) U.S. Patent No. 5,605,662.)
25

In another embodiment of the invention, nucleic acid sequences encoding PPRG may be used to generate hybridization probes useful in mapping the naturally occurring genomic sequence. The sequences may be mapped to a particular chromosome, to a specific region of a chromosome, or to artificial chromosome constructions, e.g., human artificial chromosomes
30 (HACs), yeast artificial chromosomes (YACs), bacterial artificial chromosomes (BACs), bacterial P1 constructions, or single chromosome cDNA libraries. (See, e.g., Harrington, J.J. et al. (1997) *Nat. Genet.* 15:345-355; Price, C.M. (1993) *Blood Rev.* 7:127-134; and Trask, B.J. (1991) *Trends Genet.* 7:149-154.)

Fluorescent in situ hybridization (FISH) may be correlated with other physical

chromosome mapping techniques and genetic map data. (See, e.g., Heinz-Ulrich, et al. (1995) in Meyers, supra, pp. 965-968.) Examples of genetic map data can be found in various scientific journals or at the Online Mendelian Inheritance in Man (OMIM) site. Correlation between the location of the gene encoding PPRG on a physical chromosomal map and a specific disorder, or a predisposition to a specific disorder, may help define the region of DNA associated with that disorder. The nucleotide sequences of the invention may be used to detect differences in gene sequences among normal, carrier, and affected individuals.

In situ hybridization of chromosomal preparations and physical mapping techniques, such as linkage analysis using established chromosomal markers, may be used for extending genetic maps. Often the placement of a gene on the chromosome of another mammalian species, such as mouse, may reveal associated markers even if the number or arm of a particular human chromosome is not known. New sequences can be assigned to chromosomal arms by physical mapping. This provides valuable information to investigators searching for disease genes using positional cloning or other gene discovery techniques. Once the disease or syndrome has been crudely localized by genetic linkage to a particular genomic region, e.g., ataxia-telangiectasia to 11q22-23, any sequences mapping to that area may represent associated or regulatory genes for further investigation. (See, e.g., Gatti, R.A. et al. (1988) Nature 336:577-580.) The nucleotide sequence of the subject invention may also be used to detect differences in the chromosomal location due to translocation, inversion, etc., among normal, carrier, or affected individuals.

In another embodiment of the invention, PPRG, its catalytic or immunogenic fragments, or oligopeptides thereof can be used for screening libraries of compounds in any of a variety of drug screening techniques. The fragment employed in such screening may be free in solution, affixed to a solid support, borne on a cell surface, or located intracellularly. The formation of binding complexes between PPRG and the agent being tested may be measured.

Another technique for drug screening provides for high throughput screening of compounds having suitable binding affinity to the protein of interest. (See, e.g., Geysen, et al. (1984) PCT application WO84/03564.) In this method, large numbers of different small test compounds are synthesized on a solid substrate. The test compounds are reacted with PPRG, or fragments thereof, and washed. Bound PPRG is then detected by methods well known in the art. Purified PPRG can also be coated directly onto plates for use in the aforementioned drug screening techniques. Alternatively, non-neutralizing antibodies can be used to capture the peptide and immobilize it on a solid support.

In another embodiment, one may use competitive drug screening assays in which neutralizing antibodies capable of binding PPRG specifically compete with a test compound for

binding PPRG. In this manner, antibodies can be used to detect the presence of any peptide which shares one or more antigenic determinants with PPRG.

In additional embodiments, the nucleotide sequences which encode PPRG may be used in any molecular biology techniques that have yet to be developed, provided the new techniques rely on properties of nucleotide sequences that are currently known, including, but not limited to, such properties as the triplet genetic code and specific base pair interactions.

Without further elaboration, it is believed that one skilled in the art can, using the preceding description, utilize the present invention to its fullest extent. The following preferred specific embodiments are, therefore, to be construed as merely illustrative, and not limitative of the remainder of the disclosure in any way whatsoever.

The disclosures of all patents, applications, and publications mentioned above and below, in particular U.S. Ser. No. 60/096,114 and U.S. Ser. No. 60/119,768, are hereby expressly incorporated by reference.

EXAMPLES

I. Construction of cDNA Libraries

RNA was purchased from Clontech or isolated from tissues described in Table 4. Some tissues were homogenized and lysed in guanidinium isothiocyanate, while others were homogenized and lysed in phenol or in a suitable mixture of denaturants, such as TRIZOL (Life Technologies), a monophasic solution of phenol and guanidine isothiocyanate. The resulting lysates were centrifuged over CsCl cushions or extracted with chloroform. RNA was precipitated from the lysates with either isopropanol or sodium acetate and ethanol, or by other routine methods.

Phenol extraction and precipitation of RNA were repeated as necessary to increase RNA purity. In some cases, RNA was treated with DNase. For most libraries, poly(A+) RNA was isolated using oligo d(T)-coupled paramagnetic particles (Promega), OLIGOTEX latex particles (QIAGEN, Chatsworth CA), or an OLIGOTEX mRNA purification kit (QIAGEN). Alternatively, RNA was isolated directly from tissue lysates using other RNA isolation kits, e.g., the POLY(A)PURE mRNA purification kit (Ambion, Austin TX).

In some cases, Stratagene was provided with RNA and constructed the corresponding cDNA libraries. Otherwise, cDNA was synthesized and cDNA libraries were constructed with the UNIZAP vector system (Stratagene) or SUPERScript plasmid system (Life Technologies),

using the recommended procedures or similar methods known in the art. (See, e.g., Ausubel, 1997, *supra*, units 5.1-6.6.) Reverse transcription was initiated using oligo d(T) or random primers. Synthetic oligonucleotide adapters were ligated to double stranded cDNA, and the cDNA was digested with the appropriate restriction enzyme or enzymes. For most libraries, the cDNA was size-selected (300-1000 bp) using SEPHACRYL S1000, SEPHAROSE CL2B, or SEPHAROSE CL4B column chromatography (Amersham Pharmacia Biotech) or preparative agarose gel electrophoresis. cDNAs were ligated into compatible restriction enzyme sites of the polylinker of a suitable plasmid, e.g., PBLUESCRIPT plasmid (Stratagene), pSPORT1 plasmid (Life Technologies), or pINCY (Incyte Pharmaceuticals, Palo Alto CA). Recombinant plasmids were transformed into competent *E. coli* cells including XL1-Blue, XL1-BlueMRF, or SOLR from Stratagene or DH5 α , DH10B, or ElectroMAX DH10B from Life Technologies.

II. Isolation of cDNA Clones

Plasmids were recovered from host cells by *in vivo* excision, using the UNIZAP vector system (Stratagene) or cell lysis. Plasmids were purified using at least one of the following: a Magic or WIZARD Minipreps DNA purification system (Promega); an AGTC Miniprep purification kit (Edge Biosystems, Gaithersburg MD); and QIAWELL 8 Plasmid, QIAWELL 8 Plus Plasmid, QIAWELL 8 Ultra Plasmid purification systems or the R.E.A.L. PREP 96 plasmid purification kit from QIAGEN. Following precipitation, plasmids were resuspended in 0.1 ml of distilled water and stored, with or without lyophilization, at 4°C.

Alternatively, plasmid DNA was amplified from host cell lysates using direct link PCR in a high-throughput format (Rao, V.B. (1994) *Anal. Biochem.* 216:1-14). Host cell lysis and thermal cycling steps were carried out in a single reaction mixture. Samples were processed and stored in 384-well plates, and the concentration of amplified plasmid DNA was quantified fluorometrically using PICOGREEN dye (Molecular Probes, Eugene OR) and a Fluoroskan II fluorescence scanner (Labsystems Oy, Helsinki, Finland).

III. Sequencing and Analysis

cDNA sequencing reactions were processed using standard methods or high-throughput instrumentation such as the ABI CATALYST 800 (Perkin-Elmer) thermal cycler or the PTC-200 thermal cycler (MJ Research) in conjunction with the HYDRA microdispenser (Robbins Scientific) or the MICROLAB 2200 (Hamilton) liquid transfer system. cDNA sequencing reactions were prepared using reagents provided by Amersham Pharmacia Biotech or supplied in ABI sequencing kits such as the ABI PRISM BIGDYE Terminator cycle sequencing ready reaction kit (Perkin-Elmer). Electrophoretic separation of cDNA sequencing reactions and detection of labeled polynucleotides were carried out using the MEGABACE 1000 DNA

sequencing system (Molecular Dynamics); the ABI PRISM 373 or 377 sequencing systems (Perkin-Elmer) in conjunction with standard ABI protocols and base calling software; or other sequence analysis systems known in the art. Reading frames within the cDNA sequences were identified using standard methods (reviewed in Ausubel, 1997, *supra*, unit 7.7). Some of the
5 cDNA sequences were selected for extension using the techniques disclosed in Example V.

The polynucleotide sequences derived from cDNA sequencing were assembled and analyzed using a combination of software programs which utilize algorithms well known to those skilled in the art. Table 5 summarizes the tools, programs, and algorithms used and provides applicable descriptions, references, and threshold parameters. The first column of Table 5 shows
10 the tools, programs, and algorithms used, the second column provides brief descriptions thereof, the third column presents appropriate references, all of which are incorporated by reference herein in their entirety, and the fourth column presents, where applicable, the scores, probability values, and other parameters used to evaluate the strength of a match between two sequences (the higher the score, the greater the homology between two sequences). Sequences were analyzed using
15 MACDNASIS PRO software (Hitachi Software Engineering, South San Francisco CA) and LASERGENE software (DNASTAR).

The polynucleotide sequences were validated by removing vector, linker, and polyA sequences and by masking ambiguous bases, using algorithms and programs based on BLAST, dynamic programming, and dinucleotide nearest neighbor analysis. The sequences were then
20 queried against a selection of public databases such as the GenBank primate, rodent, mammalian, vertebrate, and eukaryote databases, and BLOCKS to acquire annotation using programs based on BLAST, FASTA, and BLIMPS. The sequences were assembled into full length polynucleotide sequences using programs based on Phred, Phrap, and Consed, and were screened for open reading frames using programs based on GeneMark, BLAST, and FASTA. The full length
25 polynucleotide sequences were translated to derive the corresponding full length amino acid sequences, and these full length sequences were subsequently analyzed by querying against databases such as the GenBank databases (described above), SwissProt, BLOCKS, PRINTS, Prosite, and Hidden Markov Model (HMM)-based protein family databases such as PFAM. HMM is a probabilistic approach which analyzes consensus primary structures of gene families.
30 (See, e.g., Eddy, S.R. (1996) *Curr. Opin. Struct. Biol.* 6:361-365.)

The programs described above for the assembly and analysis of full length polynucleotide and amino acid sequences were also used to identify polynucleotide sequence fragments from SEQ ID NO:21-40. Fragments from about 20 to about 4000 nucleotides which are useful in hybridization and amplification technologies were described in The Invention section above.

IV. Northern Analysis

Northern analysis is a laboratory technique used to detect the presence of a transcript of a gene and involves the hybridization of a labeled nucleotide sequence to a membrane on which RNAs from a particular cell type or tissue have been bound. (See, e.g., Sambrook, supra, ch. 7;

5 Ausubel, 1995, supra, ch. 4 and 16.)

Analogous computer techniques applying BLAST were used to search for identical or related molecules in nucleotide databases such as GenBank or LIFESEQ (Incyte Pharmaceuticals). This analysis is much faster than multiple membrane-based hybridizations. In addition, the sensitivity of the computer search can be modified to determine whether any particular match is

10 categorized as exact or similar. The basis of the search is the product score, which is defined as:

$$\frac{\% \text{ sequence identity} \times \% \text{ maximum BLAST score}}{100}$$

The product score takes into account both the degree of similarity between two sequences and the length of the sequence match. For example, with a product score of 40, the match will be exact

15 within a 1% to 2% error, and, with a product score of 70, the match will be exact. Similar molecules are usually identified by selecting those which show product scores between 15 and 40, although lower scores may identify related molecules.

The results of northern analyses are reported as a percentage distribution of libraries in which the transcript encoding PPRG occurred. Analysis involved the categorization of cDNA

20 libraries by organ/tissue and disease. The organ/tissue categories included cardiovascular, dermatologic, developmental, endocrine, gastrointestinal, hematopoietic/immune, musculoskeletal, nervous, reproductive, and urologic. The disease/condition categories included cancer, inflammation/trauma, cell proliferation, neurological, and pooled. For each category, the number of libraries expressing the sequence of interest was counted and divided by the total number of

25 libraries across all categories. Percentage values of tissue-specific and disease- or condition-specific expression are reported in Table 3.

V. Extension of PPRG Encoding Polynucleotides

The full length nucleic acid sequences of SEQ ID NO:21-27 were produced by extension

30 of an appropriate fragment of the full length molecule using oligonucleotide primers designed from this fragment. For each nucleic acid sequence, one primer was synthesized to initiate extension of an antisense polynucleotide, and the other was synthesized to initiate extension of a sense polynucleotide. Primers were used to facilitate the extension of the known sequence "outward" generating amplicons containing new unknown nucleotide sequence for the region of

interest. The initial primers were designed from the cDNA using OLIGO 4.06 (National Biosciences), or another appropriate program, to be about 22 to 30 nucleotides in length, to have a GC content of about 50% or more, and to anneal to the target sequence at temperatures of about 68°C to about 72°C. Any stretch of nucleotides which would result in hairpin structures and primer-primer dimerizations was avoided.

Selected human cDNA libraries (Life Technologies) were used to extend the sequence. If more than one extension is necessary or desired, additional sets of primers are designed to further extend the known region.

High fidelity amplification was obtained by following the instructions for the XL-PCR kit (Perkin-Elmer) and thoroughly mixing the enzyme and reaction mix. PCR was performed using the PTC200 thermal cycler (M.J. Research) beginning with 40 pmol of each primer and the recommended concentrations of all other components of the kit, with the following parameters:

	Step 1	94°C for 1 min (initial denaturation)
	Step 2	65°C for 1 min
15	Step 3	68°C for 6 min
	Step 4	94°C for 15 sec
	Step 5	65°C for 1 min
	Step 6	68°C for 7 min
	Step 7	Repeat steps 4-6 for an additional 15 cycles
20	Step 8	94°C for 15 sec
	Step 9	65°C for 1 min
	Step 10	68°C for 7:15 min
	Step 11	Repeat steps 8-10 for an additional 12 cycles
	Step 12	72°C for 8 min
25	Step 13	4°C (and holding)

A 5 µl to 10 µl aliquot of the reaction mixture was analyzed by electrophoresis on a low concentration (about 0.6% to 0.8%) agarose mini-gel to determine which reactions were successful in extending the sequence. Bands thought to contain the largest products were excised from the gel, purified using the QIAQUICK kit (QIAGEN), and trimmed of overhangs using Klenow enzyme to facilitate religation and cloning.

After ethanol precipitation, the products were redissolved in 13 µl of ligation buffer, 1 µl T4-DNA ligase (15 units) and 1 µl T4 polynucleotide kinase were added, and the mixture was incubated at room temperature for 2 to 3 hours, or overnight at 16°C. Competent *E. coli* cells (in 40 µl of appropriate media) were transformed with 3 µl of ligation mixture and cultured in 80 µl of SOC medium. (See, e.g., Sambrook, *supra*, Appendix A, p. 2.) After incubation for one hour at 37°C, the *E. coli* mixture was plated on Luria Bertani (LB) agar (See, e.g., Sambrook, *supra*, Appendix A, p. 1) containing carbenicillin (2x carb). The following day, several colonies were randomly picked from each plate and cultured in 150 µl of liquid LB/2x carb medium placed in an

individual well of an appropriate commercially-available sterile 96-well microtiter plate. The following day, 5 μ l of each overnight culture was transferred into a non-sterile 96-well plate and, after dilution 1:10 with water, 5 μ l from each sample was transferred into a PCR array.

For PCR amplification, 18 μ l of concentrated PCR reaction mix (3.3x) containing 4 units of rTth DNA polymerase, a vector primer, and one or both of the gene-specific primers used for the extension reaction were added to each well. Amplification was performed using the following conditions:

	Step 1	94°C for 60 sec
	Step 2	94°C for 20 sec
10	Step 3	55°C for 30 sec
	Step 4	72°C for 90 sec
	Step 5	Repeat steps 2-4 for an additional 29 cycles
	Step 6	72°C for 180 sec
15	Step 7	4°C (and holding)

Aliquots of the PCR reactions were run on agarose gels together with molecular weight markers. The sizes of the PCR products were compared to the original partial cDNAs, and appropriate clones were selected, ligated into plasmid, and sequenced.

In like manner, the nucleotide sequence of SEQ ID NO:21-27 are used to obtain 5' regulatory sequences using the procedure above, oligonucleotides designed for 5' extension, and an appropriate genomic library.

The full length nucleic acid sequences of SEQ ID NO:28-40 were produced by extension of an appropriate fragment of the full length molecule using oligonucleotide primers designed from this fragment. One primer was synthesized to initiate 5' extension of the known fragment, and the other primer to initiate 3' extension of the known fragment. The initial primers were designed using OLIGO 4.06 software (National Biosciences), or another appropriate program, to be about 22 to 30 nucleotides in length, to have a GC content of about 50% or more, and to anneal to the target sequence at temperatures of about 68°C to about 72°C. Any stretch of nucleotides which would result in hairpin structures and primer-primer dimerizations was avoided.

Selected human cDNA libraries were used to extend the sequence. If more than one extension was necessary or desired, additional or nested sets of primers were designed.

High fidelity amplification was obtained by PCR using methods well known in the art. PCR was performed in 96-well plates using the PTC-200 thermal cycler (MJ Research, Inc.). The reaction mix contained DNA template, 200 nmol of each primer, reaction buffer containing Mg^{2+} , $(NH_4)_2SO_4$, and β -mercaptoethanol, Taq DNA polymerase (Amersham Pharmacia Biotech), ELONGASE enzyme (Life Technologies), and Pfu DNA polymerase (Stratagene), with the following parameters for primer pair PCI A and PCI B: Step 1: 94°C, 3 min; Step 2: 94°C, 15 sec;

Step 3: 60°C, 1 min; Step 4: 68°C, 2 min; Step 5: Steps 2, 3, and 4 repeated 20 times; Step 6: 68°C, 5 min; Step 7: storage at 4°C. In the alternative, the parameters for primer pair T7 and SK+ were as follows: Step 1: 94°C, 3 min; Step 2: 94°C, 15 sec; Step 3: 57°C, 1 min; Step 4: 68°C, 2 min; Step 5: Steps 2, 3, and 4 repeated 20 times; Step 6: 68°C, 5 min; Step 7: storage at 4°C.

5 The concentration of DNA in each well was determined by dispensing 100 µl PICOGREEN quantitation reagent (0.25% (v/v) PICOGREEN; Molecular Probes, Eugene OR) dissolved in 1X TE and 0.5 µl of undiluted PCR product into each well of an opaque fluorimeter plate (Corning Costar, Acton MA), allowing the DNA to bind to the reagent. The plate was scanned in a Fluoroskan II (Labsystems Oy, Helsinki, Finland) to measure the fluorescence of the
10 sample and to quantify the concentration of DNA. A 5 µl to 10 µl aliquot of the reaction mixture was analyzed by electrophoresis on a 1 % agarose mini-gel to determine which reactions were successful in extending the sequence.

 The extended nucleotides were desalted and concentrated, transferred to 384-well plates, digested with CviJI cholera virus endonuclease (Molecular Biology Research, Madison WI), and
15 sonicated or sheared prior to religation into pUC 18 vector (Amersham Pharmacia Biotech). For shotgun sequencing, the digested nucleotides were separated on low concentration (0.6 to 0.8%) agarose gels, fragments were excised, and agar digested with Agar ACE (Promega). Extended clones were religated using T4 ligase (New England Biolabs, Beverly MA) into pUC 18 vector (Amersham Pharmacia Biotech), treated with Pfu DNA polymerase (Stratagene) to fill-in
20 restriction site overhangs, and transfected into competent *E. coli* cells. Transformed cells were selected on antibiotic-containing media, individual colonies were picked and cultured overnight at 37°C in 384-well plates in LB/2x carb liquid media.

 The cells were lysed, and DNA was amplified by PCR using Taq DNA polymerase (Amersham Pharmacia Biotech) and Pfu DNA polymerase (Stratagene) with the following
25 parameters: Step 1: 94°C, 3 min; Step 2: 94°C, 15 sec; Step 3: 60°C, 1 min; Step 4: 72°C, 2 min; Step 5: steps 2, 3, and 4 repeated 29 times; Step 6: 72°C, 5 min; Step 7: storage at 4°C. DNA was quantified by PICOGREEN reagent (Molecular Probes) as described above. Samples with low DNA recoveries were reamplified using the same conditions as described above. Samples were diluted with 20% dimethylsulphoxide (1:2, v/v), and sequenced using DYENAMIC energy transfer
30 sequencing primers and the DYENAMIC DIRECT kit (Amersham Pharmacia Biotech) or the ABI PRISM BIGDYE Terminator cycle sequencing ready reaction kit (Perkin-Elmer).

 In like manner, the nucleotide sequences of SEQ ID NO:28-40 are used to obtain 5' regulatory sequences using the procedure above, oligonucleotides designed for such extension, and an appropriate genomic library.

VI. Labeling and Use of Individual Hybridization Probes

Hybridization probes derived from SEQ ID NO:21-40 are employed to screen cDNAs, genomic DNAs, or mRNAs. Although the labeling of oligonucleotides, consisting of about 20 base pairs, is specifically described, essentially the same procedure is used with larger nucleotide fragments. Oligonucleotides are designed using state-of-the-art software such as OLIGO 4.06 software (National Biosciences) and labeled by combining 50 pmol of each oligomer, 250 μ Ci of [γ - 32 P] adenosine triphosphate (Amersham Pharmacia Biotech), and T4 polynucleotide kinase (DuPont NEN, Boston MA). The labeled oligonucleotides are substantially purified using a SEPHADEX G-25 superfine size exclusion dextran bead column (Amersham Pharmacia Biotech).

10 An aliquot containing 10^7 counts per minute of the labeled probe is used in a typical membrane-based hybridization analysis of human genomic DNA digested with one of the following endonucleases: Ase I, Bgl II, Eco RI, Pst I, Xba I, or Pvu II (DuPont NEN).

The DNA from each digest is fractionated on a 0.7% agarose gel and transferred to nylon membranes (Nytran Plus, Schleicher & Schuell, Durham NH). Hybridization is carried out for 16 hours at 40°C. To remove nonspecific signals, blots are sequentially washed at room temperature under increasingly stringent conditions up to 0.1 x saline sodium citrate and 0.5% sodium dodecyl sulfate. Hybridization patterns are visualized using autoradiography and compared.

VII. Microarrays

A chemical coupling procedure and an ink jet device can be used to synthesize array elements on the surface of a substrate. (See, e.g., Baldeschweiler, *supra*.) An array analogous to a dot or slot blot may also be used to arrange and link elements to the surface of a substrate using thermal, UV, chemical, or mechanical bonding procedures. A typical array may be produced by hand or using available methods and machines and contain any appropriate number of elements. After hybridization, nonhybridized probes are removed and a scanner used to determine the levels and patterns of fluorescence. The degree of complementarity and the relative abundance of each probe which hybridizes to an element on the microarray may be assessed through analysis of the scanned images.

Full-length cDNAs, Expressed Sequence Tags (ESTs), or fragments thereof may comprise the elements of the microarray. Fragments suitable for hybridization can be selected using software well known in the art such as LASERGENE software (DNASTAR). Full-length cDNAs, ESTs, or fragments thereof corresponding to one of the nucleotide sequences of the present invention, or selected at random from a cDNA library relevant to the present invention, are arranged on an appropriate substrate, e.g., a glass slide. The cDNA is fixed to the slide using, e.g., UV cross-linking followed by thermal and chemical treatments and subsequent drying. (See, e.g.,

Schena, M. et al. (1995) Science 270:467-470; Shalon, D. et al. (1996) Genome Res. 6:639-645.) Fluorescent probes are prepared and used for hybridization to the elements on the substrate. The substrate is analyzed by procedures described above.

VIII. Complementary Polynucleotides

5 Sequences complementary to the PPRG-encoding sequences, or any parts thereof, are used to detect, decrease, or inhibit expression of naturally occurring PPRG. Although use of oligonucleotides comprising from about 15 to 30 base pairs is described, essentially the same procedure is used with smaller or with larger sequence fragments. Appropriate oligonucleotides are designed using OLIGO 4.06 software (National Biosciences) and the coding sequence of
10 PPRG. To inhibit transcription, a complementary oligonucleotide is designed from the most unique 5' sequence and used to prevent promoter binding to the coding sequence. To inhibit translation, a complementary oligonucleotide is designed to prevent ribosomal binding to the PPRG-encoding transcript.

IX. Expression of PPRG

15 Expression and purification of PPRG is achieved using bacterial or virus-based expression systems. For expression of PPRG in bacteria, cDNA is subcloned into an appropriate vector containing an antibiotic resistance gene and an inducible promoter that directs high levels of cDNA transcription. Examples of such promoters include, but are not limited to, the *trp-lac* (*tac*) hybrid promoter and the T5 or T7 bacteriophage promoter in conjunction with the *lac*
20 operator regulatory element. Recombinant vectors are transformed into suitable bacterial hosts, e.g., BL21(DE3). Antibiotic resistant bacteria express PPRG upon induction with isopropyl beta-D-thiogalactopyranoside (IPTG). Expression of PPRG in eukaryotic cells is achieved by infecting insect or mammalian cell lines with recombinant Autographica californica nuclear polyhedrosis virus (AcMNPV), commonly known as baculovirus. The nonessential polyhedrin gene of
25 baculovirus is replaced with cDNA encoding PPRG by either homologous recombination or bacterial-mediated transposition involving transfer plasmid intermediates. Viral infectivity is maintained and the strong polyhedrin promoter drives high levels of cDNA transcription. Recombinant baculovirus is used to infect Spodoptera frugiperda (Sf9) insect cells in most cases, or human hepatocytes, in some cases. Infection of the latter requires additional genetic
30 modifications to baculovirus. (See Engelhard, E.K. et al. (1994) Proc. Natl. Acad. Sci. U.S.A. 91:3224-3227; Sandig, V. et al. (1996) Hum. Gene Ther. 7:1937-1945.)

In most expression systems, PPRG is synthesized as a fusion protein with, e.g., glutathione S-transferase (GST) or a peptide epitope tag, such as FLAG or 6-His, permitting rapid, single-step, affinity-based purification of recombinant fusion protein from crude cell lysates.

GST, a 26-kilodalton enzyme from Schistosoma japonicum, enables the purification of fusion proteins on immobilized glutathione under conditions that maintain protein activity and antigenicity (Amersham Pharmacia Biotech). Following purification, the GST moiety can be proteolytically cleaved from PPRG at specifically engineered sites. FLAG, an 8-amino acid peptide, enables immunoaffinity purification using commercially available monoclonal and polyclonal anti-FLAG antibodies (Eastman Kodak). 6-His, a stretch of six consecutive histidine residues, enables purification on metal-chelate resins (QIAGEN). Methods for protein expression and purification are discussed in Ausubel (1995, supra, ch 10 and 16). Purified PPRG obtained by these methods can be used directly in the following activity assay.

10 **X. Demonstration of PPRG Activity**

Protease activity of PPRG is measured by the hydrolysis of appropriate synthetic peptide substrates conjugated with various chromogenic molecules in which the degree of hydrolysis is quantified by spectrophotometric (or fluorometric) absorption of the released chromophore. (Beynon, R.J. and J.S. Bond (1994) Proteolytic Enzymes: A Practical Approach, Oxford University Press, New York NY, pp.25-55.) Peptide substrates are designed according to the category of protease activity as endopeptidase (serine, cysteine, aspartic proteases), aminopeptidase (leucine aminopeptidase), or carboxypeptidase (Carboxypeptidase A and B, procollagen C-proteinase). Chromogens commonly used are 2-naphthylamine, 4-nitroaniline, and furylacrylic acid. Assays are performed at ambient temperature and contain an aliquot of the enzyme and the appropriate substrate in a suitable buffer. Reactions are carried out in an optical cuvette and followed by measurement of the increase/decrease in absorbance of the chromogen released during hydrolysis of the peptide substrate. The change in absorbance is proportional to the enzyme activity in the assay.

Regulation of protease activity (agonism or antagonism) by PPRG is measured using an appropriate protease assay as described above in the presence or absence of PPRG as an agonist or inhibitor of this activity. Protease activity is measured in the absence of PPRG (control activity) and in the presence of varying amounts of PPRG. The change in protease activity compared to the control is proportional to the amount of PPRG in the assay and is a measure of the protease regulatory activity of PPRG.

For example, for inhibitory activity of PPRG-2, the assay is carried out as described above for PPRG using a calcium activated protease, such as calpain, assayed in the absence and in the presence of various concentrations of PPRG-2. Inhibition of calpain protease activity is proportional to the activity of PPRG-2 in the assay. Similarly, for inhibitory activity of PPRG-4 and PPRG-9, assays are carried out as described above for PPRG using pancreatic trypsin assayed

in the absence and in the presence of various concentrations of PPRG-4 or PPRG-9. Inhibition of pancreatic trypsin protease activity is proportional to the activity of PPRG-4 or PPRG-9 in the assay.

XL Functional Assays

5 PPRG function is assessed by expressing the sequences encoding PPRG at physiologically elevated levels in mammalian cell culture systems. cDNA is subcloned into a mammalian expression vector containing a strong promoter that drives high levels of cDNA expression. Vectors of choice include pCMV SPORT (Life Technologies) and pCR3.1 (Invitrogen, Carlsbad CA), both of which contain the cytomegalovirus promoter. 5-10 μ g of
10 recombinant vector are transiently transfected into a human cell line, preferably of endothelial or hematopoietic origin, using either liposome formulations or electroporation. 1-2 μ g of an additional plasmid containing sequences encoding a marker protein are co-transfected. Expression of a marker protein provides a means to distinguish transfected cells from nontransfected cells and is a reliable predictor of cDNA expression from the recombinant vector. Marker proteins of
15 choice include, e.g., Green Fluorescent Protein (GFP; Clontech), CD64, or a CD64-GFP fusion protein. Flow cytometry (FCM), an automated, laser optics-based technique, is used to identify transfected cells expressing GFP or CD64-GFP and to evaluate the apoptotic state of the cells and other cellular properties. FCM detects and quantifies the uptake of fluorescent molecules that
20 diagnose events preceding or coincident with cell death. These events include changes in nuclear DNA content as measured by staining of DNA with propidium iodide; changes in cell size and granularity as measured by forward light scatter and 90 degree side light scatter; down-regulation of DNA synthesis as measured by decrease in bromodeoxyuridine uptake; alterations in expression of cell surface and intracellular proteins as measured by reactivity with specific
25 antibodies; and alterations in plasma membrane composition as measured by the binding of fluorescein-conjugated Annexin V protein to the cell surface. Methods in flow cytometry are discussed in Ormerod, M.G. (1994) Flow Cytometry, Oxford, New York NY.

The influence of PPRG on gene expression can be assessed using highly purified populations of cells transfected with sequences encoding PPRG and either CD64 or CD64-GFP. CD64 and CD64-GFP are expressed on the surface of transfected cells and bind to conserved
30 regions of human immunoglobulin G (IgG). Transfected cells are efficiently separated from nontransfected cells using magnetic beads coated with either human IgG or antibody against CD64 (DYNAL, Lake Success NY). mRNA can be purified from the cells using methods well known by those of skill in the art. Expression of mRNA encoding PPRG and other genes of interest can be analyzed by northern analysis or microarray techniques.

XII. Production of PPRG Specific Antibodies

PPRG substantially purified using polyacrylamide gel electrophoresis (PAGE; see, e.g., Harrington, M.G. (1990) *Methods Enzymol.* 182:488-495), or other purification techniques, is used to immunize rabbits and to produce antibodies using standard protocols.

5 Alternatively, the PPRG amino acid sequence is analyzed using LASERGENE software (DNASTAR) to determine regions of high immunogenicity, and a corresponding oligopeptide is synthesized and used to raise antibodies by means known to those of skill in the art. Methods for selection of appropriate epitopes, such as those near the C-terminus or in hydrophilic regions are well described in the art. (See, e.g., Ausubel, 1995, *supra*, ch. 11.)

10 Typically, oligopeptides 15 residues in length are synthesized using an ABI 431A peptide synthesizer (Perkin-Elmer) using fmoc-chemistry and coupled to KLH (Sigma-Aldrich, St. Louis MO) by reaction with N-maleimidobenzoyl-N-hydroxysuccinimide ester (MBS) to increase immunogenicity. (See, e.g., Ausubel, 1995, *supra*.) Rabbits are immunized with the oligopeptide-KLH complex in complete Freund's adjuvant. Resulting antisera are tested for antipeptide activity
15 by, for example, binding the peptide to plastic, blocking with 1% BSA, reacting with rabbit antisera, washing, and reacting with radio-iodinated goat anti-rabbit IgG.

XIII. Purification of Naturally Occurring PPRG Using Specific Antibodies

Naturally occurring or recombinant PPRG is substantially purified by immunoaffinity chromatography using antibodies specific for PPRG. An immunoaffinity column is constructed by
20 covalently coupling anti-PPRG antibody to an activated chromatographic resin, such as CNBr-activated SEPHAROSE (Amersham Pharmacia Biotech). After the coupling, the resin is blocked and washed according to the manufacturer's instructions.

Media containing PPRG are passed over the immunoaffinity column, and the column is washed under conditions that allow the preferential absorbance of PPRG (e.g., high ionic strength
25 buffers in the presence of detergent). The column is eluted under conditions that disrupt antibody/PPRG binding (e.g., a buffer of pH 2 to pH 3, or a high concentration of a chaotrope, such as urea or thiocyanate ion), and PPRG is collected.

XIV. Identification of Molecules Which Interact with PPRG

PPRG, or biologically active fragments thereof, are labeled with ¹²⁵I Bolton-Hunter
30 reagent. (See, e.g., Bolton, A.E. and W.M. Hunter (1973) *Biochem. J.* 133:529-539.) Candidate molecules previously arrayed in the wells of a multi-well plate are incubated with the labeled PPRG, washed, and any wells with labeled PPRG complex are assayed. Data obtained using different concentrations of PPRG are used to calculate values for the number, affinity, and association of PPRG with the candidate molecules.

Various modifications and variations of the described methods and systems of the invention will be apparent to those skilled in the art without departing from the scope and spirit of the invention. Although the invention has been described in connection with specific preferred embodiments, it should be understood that the invention as claimed should not be unduly limited
5 to such specific embodiments. Indeed, various modifications of the described modes for carrying out the invention which are obvious to those skilled in molecular biology or related fields are intended to be within the scope of the following claims.

Table 1

Polypeptide SEQ ID NO:	Nucleotide SEQ ID NO:	Clone ID	Library	Fragments
1	21	1220330	NEUTGMT01	1220330H1 (NEUTGMT01), 1220330R6 (NEUTGMT01), 3031706F6 (TLYMNOT05)
2	22	1342493	COLNTUT03	071068F1 (PLACNOB01), 1321108F6 (BLADNOT04), 1342493F6 (COLNTUT03), 1342493H1 (COLNTUT03), 1345967T6 (PROSNOT15), 1438889F1 (PANCNOT08), 1679890T7 (STOMFET01), 1800338T6 (COLNNOT27), 3217273H1 (TESTNOT07)
3	23	1698270	BLADTUT05	1698270H1 (BLADTUT05), 1374869H1 (LUNGNOT10), 312647R1 (LUNGNOT02), 386032H1 (THYMNOT02)
4	24	2012492	TESTNOT03	2004918R6 (TESTNOT03), 2004918T6 (TESTNOT03), 2011777H1 (TESTNOT03), 2012492H1 (TESTNOT03)
5	25	2309875	NGANNOT01	1597268F6 (BRAINOT14), 1682605X22C1 (PROSNOT15), 1683253X19C1 (PROSNOT15), 1685583X13C1 (PROSNOT15), 1752982H1 (LIVRTUT01), 2052808F6 (LIVRFET02), 2197089H1 (SPLNFET02), 856284R1 (NGANNOT01), 2309875H1 (NGANNOT01)
6	26	2479394	SMCANOT01	2479394F6 (SMCANOT01), 2479394H1 (SMCANOT01), 2623972X42F1 (KERANOT02), SAEC10649F1, SAEA03168R1, SAEC11168F1, SAEA00641R1, SAEC10266F1, SAEC11328F1
7	27	2613215	SINIUCT01	231698R1 (SINTNOT02), 1363780F1 (LUNGNOT12), 1546635R6 (PROSTUT04), 1662163F6 (BRSTNOT09), 1859908F6 (PROSNOT18), 2192713X13F1 (THYRTUT03), 2192713X15F1 (THYRTUT03), 2543078X303F1 (UTRSNOT11), 2613215H1 (SINIUCT01)
8	28	001528	U937NOT01	001528F1 (U937NOT01), 001528H1 (U937NOT01), 001528X5 (U937NOT01), 001528X6 (U937NOT01), 001528X9 (U937NOT01), 443686R6 (MPHGNOT03), 2596612H1 (OVRTUT02), 2888384X12F1 (LUNGFET04), 3598232H1 (FIBPNOT01), 4906930H2 (TLYMNOT08)
9	29	998626	KIDNTUT01	998626H1 (KIDNTUT01), 998626R6 (KIDNTUT01), 4073122F6 (KIDNTUT26)

Table 1 (cont.)

Polypeptide SEQ ID NO:	Nucleotide SEQ ID NO:	Clone ID	Library	Fragments
10	30	1393301	THYRN0T03	1393301H1 (THYRN0T03), 2008519T6 (TESTN0T03), SBFA01183F1, SBFA01807F1, SBFA03248F1, SBFA00528F1
11	31	1444055	THYRN0T03	1444055H1 (THYRN0T03), 1444055R1 (THYRN0T03), 2738343H1 (OVARN0T09)
12	32	1650177	PROSTUT09	1616250F6 (BRAITUT12), 1616250T6 (BRAITUT12), 1650177F6 (PROSTUT09), 1650177H1 (PROSTUT09), 2372255H1 (ADREN0T07), 3286138F6 (HEAON0T05), 4012302H1 (MUSCNOT10), SAEA00123F1
13	33	1902576	OVARN0T07	1902576H1 (OVARN0T07), 2909961H1 (KIDNTUT15), SZAP00669V1, SZAP02354V1, SZAP00959V1, SZAP01377V1, SZAP00432V1, SZAP00726V1, SZAP01982V1
14	34	2024210	KERAN0T02	2024210H1 (KERAN0T02), 4569479H1 (HELATXT01), 4817326H1 (HELATXT03)
15	35	2523109	BRAITUT21	2523109H1 (BRAITUT21), 3574330H1 (BRONN0T01), 3126142H1 (LUNGUTUT12), 3417837H2 (PTHYN0T04), 2309843X13C1 (NGANN0T01), 2365785X305D1 (ADREN0T07), 2674631F6 (KIDNN0T19), 4770421H1 (BRATN0T02), 2122564F6 (BRSTN0T07), 5401752H1 (BRAHN0T01), 2196601F6 (SPLNFET02), 2599102F6 (UTRSN0T10), 3030634T6 (HEARFET02), 1721515T6 (BLADN0T06), 546753F1 (BEPIN0T01)
16	36	2588566	LUNGN0T22	2588566H1 (LUNGN0T22), 2588566X303D1 (LUNGN0T22), 2727313T6 (OVARTUT05), 3972055H1 (ADRETUT06), SBKA00529F1

Table 1 (cont.)

Polypeptide SEQ ID NO:	Nucleotide SEQ ID NO:	Clone ID	Library	Fragments
17	37	2740570	BRSTTUT14	102671F1 (ADRENOR01), 102671R1 (ADRENOR01), 678618X16 (UTRSNOT02), 1259309F6 (MENITUT03), 1466058F6 (PANCUT02), 2740570H1 (BRSTTUT14), 2740570X316D2 (BRSTTUT14), 2740570X319F1 (BRSTTUT14), 3050368H1 (LUNGNOT25), SCJA02363V1
18	38	2820384	BRSTNOT14	1642163F6 (HEARFET01), 1706505F6 (DUODNOT02), 1742853T6 (HIPONON01), 1853454F6 (LUNGFET03), 1878661F6 (LEUKNOT03), 1878661H1 (LEUKNOT03), 2820384H1 (BRSTNOT14), 2820384X13F1 (BRSTNOT14), 3497393H1 (PROSTUT13), 3633187H1 (LIVRNOT03), 4059719H1 (BRAINOT21), 4144331H1 (BRSTTMT01), 4982538H1 (HELATXT05)
19	39	2990692	KIDNFET02	2990692F6 (KIDNFET02), 2990692H1 (KIDNFET02), 2990692X14F1 (KIDNFET02), 2990692X34F1 (KIDNFET02), 4636147H1 (MYEPTXT01)
20	40	4590384	MASTTXXT01	1487107F6 (UCMCL5T01), 4590384H1 (MASTTXXT01), 4918570H1 (LIVRFET05), SANA01269F1

Table 2

Polypeptide Seq ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequence	Identification	Analytical Methods
1	206	T66 S38 T103 T154 S180 T21 T31 T68 T84			Metalloproteinase	BLAST BLOCKS PRINTS
2	754	S29 T79 S188 S197 T216 T224 T235 T331 S357 T391 S410 T474 S607 S609 S709 T717 T744 S13 S42 T63 S87 S139 S167 S194 S268 T297 T313 T435 T470 S728 S741 T748 S573 T681 T687	N220 N570		Calpastatin	BLAST
3	308	S33 S136 S207 T220 S290 S304 S41 T122 S125 Y268	N144 N167	Prolyl aminopeptidase: L105 Serine protease: L66	Protease	BLOCKS PRINTS
4	164	T157		Kunitz family signature: F136	Trypsin inhibitor	BLAST BLOCKS MOTIFS PRINTS
5	565	T155 T451 S477 S115 S298 S350 T392 S415 T424 S488 T150 S156 S171 S187 S232 S415 S446 T447 S472 S494 Y195	N509 N533	Ubiquitin carboxyl- terminal hydrolase family 2 signature: Y502	Ubiquitin specific protease 41	BLAST BLOCKS MOTIFS PRINTS

Table 2 (cont.)

Polypeptide Seq ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequence	Identification	Analytical Methods
6	421	T90 S210 S284 S290 S346 S365 T401 T411 T165 T194 S321 Y310	N260	Zinc carboxy- peptidase, zinc- binding region signatures: P172, H308	Carboxypeptidase	BLAST BLOCKS MOTIFS PRINTS
7	666	T36 S97 T145 S220 T243 S257 S289 S326 S404 S450 T480 S522 T551 S619 T621 T634 S4 T199 S334 T445 S548	N132 N446		Aminopeptidase P	BLAST BLOCKS MOTIFS PRINTS
8	952	S153 S810 T105 S170 T197 S312 S513 T593 S623 S625 S636 S644 S649 T767 T821 T885 S932 T11 S23 S78 T149 S322 T329 T670 T790 Y31 Y578 Y779 Y876		Ubiquitin hydrolyase: G261-L278, Y846-V883	Ubiquitin protease	BLAST MOTIFS PFAM
9	166	S48 S119		Signal peptide: M1-A26	Trypsin inhibitor	BLAST MOTIFS SPSCAN
10	543	S505 S39 T41 S98 T134 T158 T250 S291 S331 S359 S466 T53 T59 T160 T342 S379 S399 S425 S489 Y481		Signal peptide: M1-A25	sp32 precursor, proacrosin- binding protein	BLAST MOTIFS SPSCAN

Table 2 (cont.)

Polypeptide Seq ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequence	Identification	Analytical Methods
11	83	S18 S6 S22 S40		Caspase: D15-P81	Cysteine protease	BLAST MOTIFS PFAM
12	648	S41 S132 T176 T190 T222 T242 T593 T25 S33 S64 S204 T335 T381 S472 S562 T589 S597 T630 Y263 Y310 Y508		ATP/GTP-binding site: G322-T329 Ankyrin repeat: K206-E238 Chaperonins ClpA/B: L138-I592	SKD3, regulator of Clp protease activity	BLAST MOTIFS PFAM
13	672	S99 T123 S282 S547 S568 T644 T42 T52 T110 T207 S226 T332 T488 S522 T622		Cysteine protease: Q67-A78 Calpain: L13-T322	Calcium (cysteine) protease	BLAST BLOCKS MOTIFS PFAM PRINTS
14	80	S73		Kazal-type serine protease inhibitor: C30-C80	Protease inhibitor	BLAST MOTIFS PFAM PROFILES SCAN
15	795	S418 T419 T655 S166 T278 T296 S307 S425 T427 T481 S517 S564 S639 S675 T103 S244 S330 T455 S495 S506 T556 Y138		ATP-dependent Clp protease: A345-A363 Signal peptide: M1-W23 Transmembrane domain: A254-F272	Paraplegin (metalloprotease)	BLAST MOTIFS PFAM PRINTS SPSCAN

Table 2 (cont.)

Polypeptide Seq ID NO:	Amino Acid Residues	Potential Phosphorylation Sites	Potential Glycosylation Sites	Signature Sequence	Identification	Analytical Methods
16	193	S19 S63 T182 S4 T140 T168			Neutral protease alpha subunit	BLAST MOTIFS
17	663	S437 S448 T547 T23 T27 S33 S35 S46 S98 S108 T222 S253 T289 S414 S436 T473 S481 S48 T120 S182 S347		Ubiquitin carboxyl- terminal hydrolase: Y378-V415	Ubiquitin specific protease UBP 41	BLAST MOTIFS PFAM
18	362	S130 T69 S129 T166 S40 S348 Y39		Ubiquitin carboxyl- terminal hydrolase: Y71-V108	Ubiquitin specific protease UBP 41	BLAST MOTIFS PFAM
19	210	T133 T144 T89 S199		Retroviral aspartyl protease: V111-I193	Human endogenous retroviral protease	BLAST MOTIFS PFAM
20	283	S266 S77 S94 T110 S166 S50 S191 S208 T275		Trypsin: I34-I258 Serine protease, active site: V70-C75	Metase (serine protease)	BLAST MOTIFS PFAM PROFILES CAN

Table 3

Nucleotide SEQ ID NO:	Tissue Expression (Fraction of Total)	Disease or Condition (Fraction of Total)	Vector
21	Hematopoietic/Immune (0.750) Reproductive (0.250)	Inflammation (0.750) Cancer (0.250) Fetal (0.250)	PSPORT
22	Reproductive (0.255) Gastrointestinal (0.196) Cardiovascular (0.125)	Cancer (0.475) Inflammation (0.245) Fetal (0.152)	pINCY
23	Reproductive (0.258) Cardiovascular (0.129) Gastrointestinal (0.129)	Cancer (0.419) Inflammation (0.226) Fetal (0.204)	pINCY
24	Reproductive (1.00)	Inflammation (1.000)	PBLUESCRIPT
25	Reproductive (0.258) Nervous (0.210) Gastrointestinal (0.161)	Cancer (0.548) Inflammation (0.242) Fetal (0.129)	PSPORT
26	Nervous (0.500) Cardiovascular (0.250) Dermatologic (0.250)	Cancer (0.500) Fetal (0.500)	pINCY
27	Reproductive (0.244) Gastrointestinal (0.179) Developmental (0.141)	Cancer (0.418) Fetal (0.231) Inflammation (0.154)	pINCY
28	Hematopoietic/Immune (0.304) Reproductive (0.232) Cardiovascular (0.107)	Cell proliferation (0.465) Inflammation (0.429)	PBLUESCRIPT
29	Urologic (0.714) Musculoskeletal (0.147)	Cancer (0.857) Inflammation (0.143)	PSPORT1

Table 3 (cont.)

Nucleotide SEQ ID NO:	Tissue Expression (Fraction of Total)	Disease or Condition (Fraction of Total)	Vector
30	Reproductive (0.375) Endocrine (0.125) Hematopoietic/Immune (0.250)	Inflammation (0.500) Cancer (0.375)	pINCY
31	Hematopoietic/Immune (0.308) Cardiovascular (0.154) Reproductive (0.154)	Inflammation (0.616) Cancer (0.385)	pINCY
32	Hematopoietic/Immune (0.261) Musculoskeletal (0.217) Reproductive (0.217)	Cell proliferation (0.565) Inflammation (0.435)	pINCY
33	Reproductive (0.333) Nervous (0.222)	Cell proliferation (0.703) Inflammation (0.148)	pINCY
34	Reproductive (0.600) Dermatologic (0.300) Nervous (0.100)	Cell proliferation (0.800)	PSPORT1
35	Reproductive (0.202) Nervous (0.173) Gastrointestinal (0.135)	Cell proliferation (0.586) Inflammation (0.279)	pINCY
36	Gastrointestinal (0.500) Cardiovascular (0.333) Endocrine (0.167)	Cancer (0.833) Inflammation (0.167)	pINCY
37	Nervous (0.205) Reproductive (0.205) Cardiovascular (0.179)	Cell proliferation (0.538) Inflammation (0.154)	pINCY

Table 3 (cont.)

Nucleotide SEQ ID NO:	Tissue Expression (Fraction of Total)	Disease or Condition (Fraction of Total)	Vector
38	Hematopoietic/Immune (0.267) Reproductive (0.250) Nervous (0.133)	Cell proliferation (0.600) Inflammation (0.383)	pINCY
39	Hematopoietic/Immune (0.400) Developmental (0.200) Gastrointestinal (0.200)	Cell proliferation (0.800) Inflammation (0.400)	pINCY
40	Gastrointestinal (0.500) Hematopoietic/Immune (0.500)	Cell proliferation (0.500) Inflammation (0.500)	pINCY

Table 4

Nucleotide SEQ ID NO:	Library	Library Comment
21	NEUTGMT01	Library was constructed using RNA isolated from peripheral blood granulocytes collected by density gradient centrifugation through Ficoll-Hypaque. The cells were isolated from buffy coat units obtained from 20 unrelated male and female donors. Cells were cultured in 10 nM GM-CSF for 1 hour before washing and harvesting for RNA preparation.
22	COLNTUT03	Library was constructed using RNA isolated from colon tumor tissue obtained from the sigmoid colon of a 62-year-old Caucasian male during a sigmoidectomy and permanent colostomy. Pathology indicated invasive grade 2 adenocarcinoma. One lymph node contained metastasis with extranodal extension. Patient history included hyperlipidemia, cataract disorder, and dermatitis. Family history included cardiovascular disease and cancer.
23	BLADTUT05	Library was constructed using RNA isolated from bladder tumor tissue removed from a 66-year-old Caucasian male during a radical prostatectomy, radical cystectomy, and urinary diversion. Pathology indicated grade 3 transitional cell carcinoma on the anterior wall of the bladder. Patient history included lung neoplasm and tobacco abuse in remission. Family history included a malignant breast neoplasm, tuberculosis, cerebrovascular disease, atherosclerotic coronary artery disease, and lung cancer.
24	TESTNOT03	Library was constructed using polyA RNA isolated from testicular tissue removed from a 37-year-old Caucasian male who died from liver disease. Patient history included cirrhosis, jaundice, and liver failure.
25	NGANNOT01	Library was constructed using RNA isolated from tumorous neuroganglion tissue removed from a 9-year-old Caucasian male during a soft tissue excision of the chest wall. Pathology indicated a ganglioneuroma. Family history included asthma.
26	SMCANOT01	Library was constructed using RNA isolated from an aortic smooth muscle cell line derived from the explanted heart of a male during a heart transplant.

Table 4 (cont.)

Nucleotide SEQ ID NO:	Library	Library Comment
27	SINIUCT01	Library was constructed using RNA isolated from ileum tissue obtained from a 42-year-old Caucasian male during a total intra-abdominal colectomy and endoscopic jejunostomy. Previous surgeries included polypectomy, colonoscopy, and spinal canal exploration. Family history included cerebrovascular disease, benign hypertension, atherosclerotic coronary artery disease, and type II diabetes.
28	U937NOT01	Library was constructed at Stratagene (STR937207), using RNA isolated from the U937 monocyte-like cell line. This line (ATCC CRL1593) was established from malignant cells obtained from the pleural effusion of a 37-year-old Caucasian male with diffuse histiocytic lymphoma.
29	KIDNTUT01	Library was constructed using RNA isolated from kidney tumor tissue removed from an 8-month-old female during nephroureterectomy. Pathology indicated Wilms' tumor (nephroblastoma), which involved 90 percent of the renal parenchyma. Prior to surgery, the patient was receiving heparin anticoagulant therapy.
30	THYRNOT03	Library was constructed using RNA isolated from thyroid tissue removed from the left thyroid of a 28-year-old Caucasian female during a complete thyroidectomy. Pathology indicated a small nodule of adenomatous hyperplasia present in the left thyroid. Pathology for the associated tumor tissue indicated dominant follicular adenoma forming a well-encapsulated mass in the left thyroid.
31	THYRNOT03	Library was constructed using RNA isolated from thyroid tissue removed from the left thyroid of a 28-year-old Caucasian female during a complete thyroidectomy. Pathology indicated a small nodule of adenomatous hyperplasia present in the left thyroid. Pathology for the associated tumor tissue indicated dominant follicular adenoma forming a well-encapsulated mass in the left thyroid.

Table 4 (cont.)

Nucleotide SEQ ID NO:	Library	Library Comment
32	PROSTUT09	Library was constructed using RNA isolated from prostate tumor tissue removed from a 66-year-old Caucasian male during a radical prostatectomy, radical cystectomy, and urinary diversion. Pathology indicated grade 3 transitional cell carcinoma. The patient presented with prostatic inflammatory disease. Patient history included lung neoplasm, and benign hypertension. Family history included a malignant breast neoplasm, tuberculosis, cerebrovascular disease, atherosclerotic coronary artery disease and lung cancer.
33	OVARNOT07	Library was constructed using RNA isolated from left ovarian tissue removed from a 28-year-old Caucasian female during a vaginal hysterectomy and removal of the fallopian tubes and ovaries. The tissue was associated with multiple follicular cysts, endometrium in a weakly proliferative phase, and chronic cervicitis of the cervix with squamous metaplasia. Family history included benign hypertension, hyperlipidemia, and atherosclerotic coronary artery disease.
34	KERANOT02	Library was constructed using RNA isolated from epidermal breast keratinocytes (NHEK). NHEK (Clontech #CC-2501) is human breast keratinocyte cell line derived from a 30-year-old black female during breast-reduction surgery.
35	BRAITUT21	Library was constructed using RNA isolated from brain tumor tissue removed from the midline frontal lobe of a 61-year-old Caucasian female during excision of a cerebral meningeal lesion. Pathology indicated subfrontal meningotheial meningioma with no atypia. One ethmoid and mucosal tissue sample indicated meningioma. Family history included cerebrovascular disease, senile dementia, hyperlipidemia, benign hypertension, atherosclerotic coronary artery disease, congestive heart failure, and breast cancer.
36	LUNGNOT22	Library was constructed using RNA isolated from lung tissue removed from a 58-year-old Caucasian female. The tissue sample used to construct this library was found to have tumor contaminant upon microscopic examination. Pathology for the associated tumor tissue indicated a caseating granuloma. Family history included congestive heart failure, breast cancer, secondary bone cancer, acute myocardial infarction and atherosclerotic coronary artery disease.

Table 4 (cont.)

Nucleotide SEQ ID NO:	Library	Library Comment
37	BRSTTUT14	Library was constructed using RNA isolated from breast tumor tissue removed from a 62-year-old Caucasian female during a unilateral extended simple mastectomy. Pathology indicated an invasive grade 3 (of 4), nuclear grade 3 (of 3) adenocarcinoma, ductal type. Ductal carcinoma in situ, comedo type, comprised 60% of the tumor mass. Metastatic adenocarcinoma was identified in one (of 14) axillary lymph nodes with no perinodal extension. Tumor cells were strongly positive for estrogen receptors and weakly positive for progesterone receptors. Patient history included benign colon neoplasm, hyperlipidemia, cardiac dysrhythmia, and obesity. Family history included atherosclerotic coronary artery disease, myocardial infarction, colon cancer, ovarian cancer, lung cancer, and cerebrovascular disease.
38	BRSTNOT14	Library was constructed using RNA isolated from breast tissue removed from a 62-year-old Caucasian female during a unilateral extended simple mastectomy. Pathology for the associated tumor tissue indicated an invasive grade 3 (of 4), nuclear grade 3 (of 3) adenocarcinoma, ductal type. Ductal carcinoma in situ, comedo type, comprised 60% of the tumor mass. Metastatic adenocarcinoma was identified in one (of 14) axillary lymph nodes with no perinodal extension. The tumor cells were strongly positive for estrogen receptors and weakly positive for progesterone receptors. Patient history included a benign colon neoplasm, hyperlipidemia, cardiac dysrhythmia, and obesity. Family history included atherosclerotic coronary artery disease, myocardial infarction, colon cancer, ovarian cancer, lung cancer, and cerebrovascular disease.
39	KIDNFET02	Library was constructed using RNA isolated from kidney tissue removed from a Caucasian male fetus, who was stillborn with a hypoplastic left heart at 23 weeks' gestation.
40	MASTTXT01	Library was constructed using RNA isolated from mast cells differentiated from treated CD34+ stem cells removed from the liver of a fetus who died at 22 weeks' gestation. The CD34+ stem cells were treated with hIL-6 and hSCF (human stem cell factor) for 18 days to induce differentiation.

Table 5

Program	Description	Reference	Parameter Threshold
ABI FACTURA	A program that removes vector sequences and masks ambiguous bases in nucleic acid sequences.	Perkin-Elmer Applied Biosystems, Foster City, CA.	
ABI/PARACEL FDF	A Fast Data Finder useful in comparing and annotating amino acid or nucleic acid sequences.	Perkin-Elmer Applied Biosystems, Foster City, CA; Paracel Inc., Pasadena, CA.	Mismatch <50%
ABI AutoAssembler	A program that assembles nucleic acid sequences.	Perkin-Elmer Applied Biosystems, Foster City, CA.	
BLAST	A Basic Local Alignment Search Tool useful in sequence similarity search for amino acid and nucleic acid sequences. BLAST includes five functions: blastp, blastn, blastx, tblastn, and tblastx.	Altschul, S.F. et al. (1990) J. Mol. Biol. 215:403-410; Altschul, S.F. et al. (1997) Nucleic Acids Res. 25: 3389-3402.	ESTs: Probability value= 1.0E-8 or less Full Length sequences: Probability value= 1.0E-10 or less
FASTA	A Pearson and Lipman algorithm that searches for similarity between a query sequence and a group of sequences of the same type. FASTA comprises as least five functions: fasta, ifasta, fastx, ifastx, and ssearch.	Pearson, W.R. and D.J. Lipman (1988) Proc. Natl. Acad. Sci. 85:2444-2448; Pearson, W.R. (1990) Methods Enzymol. 183: 63-98; and Smith, T.F. and M. S. Waterman (1981) Adv. Appl. Math. 2:482-489.	ESTs: fasta E value=1.06E-6 Assembled ESTs: fasta Identity= 95% or greater and Match length=200 bases or greater; fastx E value=1.0E-8 or less Full Length sequences: fastx score=100 or greater
BLIMPS	A BLocks IMProved Searcher that matches a sequence against those in BLOCKS and PRINTS databases to search for gene families, sequence homology, and structural fingerprint regions.	Henikoff, S. and J.G. Henikoff, Nucl. Acid Res. 19:6565-72, 1991. J.G. Henikoff and S. Henikoff (1996) Methods Enzymol. 266:88-105; and Attwood, T.K. et al. (1997) J. Chem. Inf. Comput. Sci. 37: 417-424.	Score=1000 or greater; Ratio of Score/Strength = 0.75 or larger; and Probability value= 1.0E-3 or less
PFAM	A Hidden Markov Models-based application useful for protein family search.	Krogh, A. et al. (1994) J. Mol. Biol., 235:1501-1531; Sonnhammer, E.L.L. et al. (1988) Nucleic Acids Res. 26:320-322.	Score=10-50 bits, depending on individual protein families

Table 5 cont.

Program	Description	Reference	Parameter Threshold
ProfileScan	An algorithm that searches for structural and sequence motifs in protein sequences that match sequence patterns defined in Prosite.	Gribskov, M. et al. (1988) CABIOS 4:61-66; Gribskov, et al. (1989) Methods Enzymol. 183:146-159; Bairoch, A. et al. (1997) Nucleic Acids Res. 25: 217-221.	Score= 4.0 or greater
Phred	A base-calling algorithm that examines automated sequencer traces with high sensitivity and probability.	Ewing, B. et al. (1998) Genome Res. 8:175-185; Ewing, B. and P. Green (1998) Genome Res. 8:186-194.	
Phrap	A Phils Revised Assembly Program including SWAT and CrossMatch, programs based on efficient implementation of the Smith-Waterman algorithm, useful in searching sequence homology and assembling DNA sequences.	Smith, T.F. and M. S. Waterman (1981) Adv. Appl. Math. 2:482-489; Smith, T.F. and M. S. Waterman (1981) J. Mol. Biol. 147:195-197; and Green, P., University of Washington, Seattle, WA.	Score= 120 or greater; Match length= 56 or greater
Consed	A graphical tool for viewing and editing Phrap assemblies	Gordon, D. et al. (1998) Genome Res. 8:195-202.	
SPScan	A weight matrix analysis program that scans protein sequences for the presence of secretory signal peptides.	Nielson, H. et al. (1997) Protein Engineering 10:1-6; Claverie, J.M. and S. Audic (1997) CABIOS 12: 431-439.	Score=5 or greater
Motifs	A program that searches amino acid sequences for patterns that matched those defined in Prosite.	Bairoch et al. <i>supra</i> ; Wisconsin Package Program Manual, version 9, page M51-59, Genetics Computer Group, Madison, WI.	

What is claimed is:

1. A substantially purified polypeptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO:1-20, and fragments thereof.
5
2. A substantially purified variant having at least 90% amino acid sequence identity to the amino acid sequence of claim 1.
3. An isolated and purified polynucleotide encoding the polypeptide of claim 1.
10
4. An isolated and purified polynucleotide variant having at least 90% polynucleotide sequence identity to the polynucleotide of claim 3.
5. An isolated and purified polynucleotide which hybridizes under stringent
15 conditions to the polynucleotide of claim 3.
6. An isolated and purified polynucleotide having a sequence which is complementary to the polynucleotide of claim 3.
- 20 7. A method for detecting a polynucleotide, the method comprising the steps of:
 - (a) hybridizing the polynucleotide of claim 6 to at least one nucleic acid in a sample, thereby forming a hybridization complex; and
 - (b) detecting the hybridization complex, wherein the presence of the hybridization complex correlates with the presence of the polynucleotide in the sample.
25
8. The method of claim 7 further comprising amplifying the polynucleotide prior to hybridization.
9. An isolated and purified polynucleotide comprising a polynucleotide sequence
30 selected from the group consisting of SEQ ID NO:21-40, and fragments thereof.
10. An isolated and purified polynucleotide variant having at least 90% polynucleotide sequence identity to the polynucleotide of claim 9.

11. An isolated and purified polynucleotide having a sequence which is complementary to the polynucleotide of claim 9.
12. An expression vector comprising at least a fragment of the polynucleotide of claim 3.
13. A host cell comprising the expression vector of claim 12.
14. A method for producing a polypeptide, the method comprising the steps of:
- a) culturing the host cell of claim 13 under conditions suitable for the expression of the polypeptide; and
- b) recovering the polypeptide from the host cell culture.
15. A pharmaceutical composition comprising the polypeptide of claim 1 in conjunction with a suitable pharmaceutical carrier.
16. A purified antibody which specifically binds to the polypeptide of claim 1.
17. A purified agonist of the polypeptide of claim 1.
18. A purified antagonist of the polypeptide of claim 1.
19. A method for treating or preventing a disorder associated with decreased expression or activity of PPRG, the method comprising administering to a subject in need of such treatment an effective amount of the pharmaceutical composition of claim 15.
20. A method for treating or preventing a disorder associated with increased expression or activity of PPRG, the method comprising administering to a subject in need of such treatment an effective amount of the antagonist of claim 18.

SEQUENCE LISTING

<110> INCYTE PHARMACEUTICALS, INC.

BANDMAN, Olga

HILLMAN, Jennifer L.

BAUGHN, Mariah R.

AZIMZAI, Yalda

GUEGLER, Karl J.

CORLEY, Neil C.

YUE, Henry

TANG, Y. Tom

REDDY, Roopa

PATTERSON, Chandra

AU-YOUNG, Janice

SHI, Leo L.

LU, Dyung Aina M.

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Ala	Gly	Leu	Val	Arg	Arg	Arg	Arg	Tyr	Ala	Leu	Ser	Gly	Ser	
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Gln	Ser	Ser	Gln	Leu	Ser	Gln	Glu	Thr	Val	Arg	Val	Leu	Met	Ser
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Tyr	Ala	Leu	Met	Ala	Trp	Gly	Met	Glu	Ser	Gly	Leu	Thr	Phe	His
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Glu	Val	Asp	Ser	Pro	Gln	Gly	Gln	Glu	Pro	Asp	Ile	Leu	Ile	Asp

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Ser Gly Asp Thr	His Phe Asp Asp Glu	Glu Thr Trp Thr Phe	Gly		
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Ser Lys Ala Ser	Gln Gln Leu Glu Gln	Glu Leu Ala Gly Gly	Ser		
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Ser Ala Ala Pro Pro Gln Glu Lys Lys Arg Lys Val Glu Lys Asp	320	325	330
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Glu Asp Asp Glu Thr Ile Pro Ser Glu Tyr Arg Leu Lys Pro Ala	380	385	390
Thr Asp Lys Asp Gly Lys Pro Leu Leu Pro Glu Pro Glu Glu Lys	395	400	405
Pro Lys Pro Arg Ser Glu Ser Glu Leu Ile Asp Glu Leu Ser Glu	410	415	420
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Val Phe Gln Lys Tyr Val Pro Ser Phe Ser Gly Tyr Ser Gln Gln		
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380	385	390
Ser Thr Thr Phe Glu Val Phe Cys Asp Leu Ser Leu Pro Ile Pro		
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Lys Lys Gly Phe Ala Gly Gly Lys Val Ser Leu Arg Asp Cys Phe		
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Lys Ala Gly Ser Pro Val Tyr Gln Leu Tyr Ala Leu Cys Asn His
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Ser Gly Ser Val His Tyr Gly His Tyr Thr Ala Leu Cys Arg Cys
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Gln Thr Gly Trp His Val Tyr Asn Asp Ser Arg Val Ser Pro Val
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  125         130         135
Ile Ala Ala Asp Phe Pro Asp Leu Ala Arg Arg Val Lys Ile Gly
  140         145         150
His Ser Phe Glu Asn Arg Pro Met Tyr Val Leu Lys Phe Ser Thr
  155         160         165
Gly Lys Gly Val Arg Arg Pro Ala Val Trp Leu Asn Ala Gly Ile
  170         175         180
His Ser Arg Glu Trp Ile Ser Gln Ala Thr Ala Ile Trp Thr Ala
  185         190         195
Arg Lys Ile Val Ser Asp Tyr Gln Arg Asp Pro Ala Ile Thr Ser
  200         205         210
Ile Leu Glu Lys Met Asp Ile Phe Leu Leu Pro Val Ala Asn Pro

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215	220	225
Asp Gly Tyr Val Tyr Thr Gln Thr Gln Asn Arg Leu Trp Arg Lys		
230	235	240
Thr Arg Ser Arg Asn Pro Gly Ser Ser Cys Ile Gly Ala Asp Pro		
245	250	255
Asn Arg Asn Trp Asn Ala Ser Phe Ala Gly Lys Gly Ala Ser Asp		
260	265	270
Asn Pro Cys Ser Glu Val Tyr His Gly Pro His Ala Asn Ser Glu		
275	280	285
Val Glu Val Lys Ser Val Val Asp Phe Ile Gln Lys His Gly Asn		
290	295	300
Phe Lys Gly Phe Ile Asp Leu His Ser Tyr Ser Gln Leu Leu Met		
305	310	315
Tyr Pro Tyr Gly Tyr Ser Val Lys Lys Ala Pro Asp Ala Glu Glu		
320	325	330
Leu Asp Lys Val Ala Arg Leu Ala Ala Lys Ala Leu Ala Ser Val		
335	340	345
Ser Gly Thr Glu Tyr Gln Val Gly Pro Thr Cys Thr Thr Val Tyr		
350	355	360
Pro Ala Ser Gly Ser Ser Ile Asp Trp Ala Tyr Asp Asn Gly Ile		
365	370	375
Lys Phe Ala Phe Thr Phe Glu Leu Arg Asp Thr Gly Thr Tyr Gly		
380	385	390
Phe Leu Leu Pro Ala Asn Gln Ile Ile Pro Thr Ala Glu Glu Thr		
395	400	405
Trp Leu Gly Leu Lys Thr Ile Met Glu His Val Arg Asp Asn Leu		
410	415	420
Tyr		

<210> 7

<211> 666

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 2613215

<400> 7

Met Ala Ala Ser Arg Lys Pro Pro Arg Val Arg Val Asn His Gln		
1	5	10
Asp Phe Gln Leu Arg Asn Leu Arg Ile Ile Glu Pro Asn Glu Val		
20	25	30
Thr His Ser Gly Asp Thr Gly Val Glu Thr Asp Gly Arg Met Pro		
35	40	45
Pro Lys Val Thr Ser Glu Leu Leu Arg Gln Leu Arg Gln Ala Met		
50	55	60
Arg Asn Ser Glu Tyr Val Thr Glu Pro Ile Gln Ala Tyr Ile Ile		
65	70	75
Pro Ser Gly Asp Ala His Gln Ser Glu Tyr Ile Ala Pro Cys Asp		
80	85	90
Cys Arg Arg Ala Phe Val Ser Gly Phe Asp Gly Ser Ala Gly Thr		
95	100	105
Ala Ile Ile Thr Glu Glu His Ala Ala Met Trp Thr Asp Gly Arg		
110	115	120
Tyr Phe Leu Gln Ala Ala Lys Gln Met Asp Ser Asn Trp Thr Leu		

Met Lys Met Gly	125	130	135
Leu Lys Asp Thr Pro		Thr Gln Glu Asp Trp	Leu
Val Ser Val Leu	140	145	150
Pro Glu Gly Ser Arg		Val Gly Val Asp Pro	Leu
Ile Ile Pro Thr	155	160	165
Asp Tyr Trp Lys Lys		Met Ala Lys Val Leu	Arg
Ser Ala Gly His	170	175	180
His Leu Ile Pro Val		Lys Glu Asn Leu Val	Asp
Lys Ile Trp Thr	185	190	195
Asp Arg Pro Glu Arg		Pro Cys Lys Pro Leu	Leu
Thr Leu Gly Leu	200	205	210
Asp Tyr Thr Gly Ile		Ser Trp Lys Asp Lys	Val
Ala Asp Leu Arg	215	220	225
Leu Lys Met Ala Glu		Arg Asn Val Met Trp	Phe
Val Val Thr Ala	230	235	240
Leu Asp Glu Ile Ala		Trp Leu Phe Asn Leu	Arg
Gly Ser Asp Val	245	250	255
Glu His Asn Pro Val		Phe Phe Ser Tyr Ala	Ile
Ile Gly Leu Glu	260	265	270
Thr Ile Met Leu Phe		Ile Asp Gly Asp Arg	Ile
Asp Ala Pro Ser	275	280	285
Val Lys Glu His Leu		Leu Leu Asp Leu Gly	Leu
Glu Ala Glu Tyr	290	295	300
Arg Ile Gln Val His		Pro Tyr Lys Ser Ile	Leu
Ser Glu Leu Lys	305	310	315
Ala Leu Cys Ala Asp		Leu Ser Pro Arg Glu	Lys
Val Trp Val Ser	320	325	330
Asp Lys Ala Ser Tyr		Ala Val Ser Glu Thr	Ile
Pro Lys Asp His	335	340	345
Arg Cys Cys Met Pro		Tyr Thr Pro Ile Cys	Ile
Ala Lys Ala Val	350	355	360
Lys Asn Ser Ala Glu		Ser Glu Gly Met Arg	Arg
Ala His Ile Lys	365	370	375
Asp Ala Val Ala Leu		Cys Glu Leu Phe Asn	Trp
Leu Glu Lys Glu	380	385	390
Val Pro Lys Gly Gly		Val Thr Glu Ile Ser	Ala
Ala Asp Lys Ala	395	400	405
Glu Glu Phe Arg Arg		Gln Gln Ala Asp Phe	Val
Asp Leu Ser Phe	410	415	420
Pro Thr Ile Ser Ser		Thr Gly Pro Asn Gly	Ala
Ile Ile His Tyr	425	430	435
Ala Pro Val Pro Glu		Thr Asn Arg Thr Leu	Ser
Leu Asp Glu Val	440	445	450
Tyr Leu Ile Asp Ser		Gly Ala Gln Tyr Lys	Asp
Gly Thr Thr Asp	455	460	465
Val Thr Arg Thr Met		His Phe Gly Thr Pro	Thr
Ala Tyr Glu Lys	470	475	480
Glu Cys Phe Thr Tyr		Val Leu Lys Gly His	Ile
Ala Val Ser Ala	485	490	495
Ala Val Phe Pro Thr		Gly Thr Lys Gly His	Leu
Leu Asp Ser Phe	500	505	510
Ala Arg Ser Ala Leu		Trp Asp Ser Gly Leu	Asp
Tyr Leu His Gly	515	520	525
Thr Gly His Gly Val		Gly Ser Phe Leu Asn	Val
His Glu Gly Pro	530	535	540
Cys Gly Ile Ser Tyr		Lys Thr Phe Ser Asp	Glu
	545	550	555

Pro Leu Glu Ala Gly Met Ile Val Thr Asp Glu Pro Gly Tyr Tyr
 560 565 570
 Glu Asp Gly Ala Phe Gly Ile Arg Ile Glu Asn Val Val Leu Val
 575 580 585
 Val Pro Val Lys Thr Lys Tyr Asn Phe Asn Asn Arg Gly Ser Leu
 590 595 600
 Thr Phe Glu Pro Leu Thr Leu Val Pro Ile Gln Thr Lys Met Ile
 605 610 615
 Asp Val Asp Ser Leu Thr Asp Lys Glu Cys Asp Trp Leu Asn Asn
 620 625 630
 Tyr His Leu Thr Cys Arg Asp Val Ile Gly Lys Glu Leu Gln Lys
 635 640 645
 Gln Gly Arg Gln Glu Ala Leu Glu Trp Leu Ile Arg Glu Thr Gln
 650 655 660
 Pro Ile Ser Lys Lys His
 665

<210> 8

<211> 952

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 001528

<400> 8

Met Ala Glu Gly Gly Ala Ala Asp Leu Asp Thr Gln Arg Ser Asp
 1 5 10 15
 Ile Ala Thr Leu Leu Lys Thr Ser Leu Arg Lys Gly Asp Thr Trp
 20 25 30
 Tyr Leu Val Asp Ser Arg Trp Phe Lys Gln Trp Lys Lys Tyr Val
 35 40 45
 Gly Phe Asp Ser Trp Asp Lys Tyr Gln Met Gly Asp Gln Asn Val
 50 55 60
 Tyr Pro Gly Pro Ile Asp Asn Ser Gly Leu Leu Lys Asp Gly Asp
 65 70 75
 Ala Gln Ser Leu Lys Glu His Leu Ile Asp Glu Leu Asp Tyr Ile
 80 85 90
 Leu Leu Pro Thr Glu Gly Trp Asn Lys Leu Val Ser Trp Tyr Thr
 95 100 105
 Leu Met Glu Gly Gln Glu Pro Ile Ala Arg Lys Val Val Glu Gln
 110 115 120
 Gly Met Phe Val Lys Arg Cys Lys Val Glu Val Tyr Leu Thr Glu
 125 130 135
 Leu Lys Leu Cys Glu Asn Gly Asn Met Asn Asn Val Val Thr Arg
 140 145 150
 Arg Phe Ser Lys Ala Asp Thr Ile Asp Thr Ile Glu Lys Glu Ile
 155 160 165
 Arg Lys Ile Phe Ser Ile Pro Asp Glu Lys Glu Thr Arg Leu Trp
 170 175 180
 Asn Lys Tyr Met Ser Asn Thr Phe Glu Pro Leu Asn Lys Pro Asp
 185 190 195
 Ser Thr Ile Gln Asp Ala Gly Leu Tyr Gln Gly Gln Val Leu Val
 200 205 210
 Ile Glu Gln Lys Asn Glu Asp Gly Thr Arg Pro Arg Gly Pro Ser

215	220	225
Thr Pro Asn Val Lys Asn Ser Asn Tyr	Cys Leu Pro Ser Tyr Thr	
230	235	240
Ala Tyr Lys Asn Tyr Asp Tyr Ser Glu	Pro Gly Arg Asn Asn Glu	
245	250	255
Gln Pro Gly Leu Cys Gly Leu Ser Asn	Leu Gly Asn Thr Cys Phe	
260	265	270
Met Asn Ser Ala Ile Gln Cys Leu Ser	Asn Thr Pro Pro Leu Thr	
275	280	285
Glu Tyr Phe Leu Asn Asp Lys Tyr Gln	Glu Glu Leu Asn Phe Asp	
290	295	300
Asn Pro Leu Gly Met Arg Gly Glu Ile	Ala Lys Ser Tyr Ala Glu	
305	310	315
Leu Ile Lys Gln Met Trp Ser Gly Lys	Phe Ser Tyr Val Thr Pro	
320	325	330
Arg Ala Phe Lys Thr Gln Val Gly Arg	Phe Ala Pro Gln Phe Ser	
335	340	345
Gly Tyr Gln Gln Gln Asp Cys Gln Glu	Leu Leu Ala Phe Leu Leu	
350	355	360
Asp Gly Leu His Glu Asp Leu Asn Arg	Ile Arg Lys Lys Pro Tyr	
365	370	375
Ile Gln Leu Lys Asp Ala Asp Gly Arg	Pro Asp Lys Val Val Ala	
380	385	390
Glu Glu Ala Trp Glu Asn His Leu Lys	Arg Asn Asp Ser Ile Ile	
395	400	405
Val Asp Ile Phe His Gly Leu Phe Lys	Ser Thr Leu Val Cys Pro	
410	415	420
Glu Cys Ala Lys Ile Ser Val Thr Phe	Asp Pro Phe Cys Tyr Leu	
425	430	435
Thr Leu Pro Leu Pro Met Lys Lys Glu	Arg Thr Leu Glu Val Tyr	
440	445	450
Leu Val Arg Met Asp Pro Leu Thr Lys	Pro Met Gln Tyr Lys Val	
455	460	465
Val Val Pro Lys Ile Gly Asn Ile Leu	Asp Leu Cys Thr Ala Leu	
470	475	480
Ser Ala Leu Ser Gly Ile Pro Ala Asp	Lys Met Ile Val Thr Asp	
485	490	495
Ile Tyr Asn His Arg Phe His Arg Ile	Phe Ala Met Asp Glu Asn	
500	505	510
Leu Ser Ser Ile Met Glu Arg Asp Asp	Ile Tyr Val Phe Glu Ile	
515	520	525
Asn Ile Asn Arg Thr Glu Asp Thr Glu	His Val Ile Ile Pro Val	
530	535	540
Cys Leu Arg Glu Lys Phe Arg His Ser	Ser Tyr Thr His His Thr	
545	550	555
Gly Ser Ser Leu Phe Gly Gln Pro Phe	Leu Met Ala Val Pro Arg	
560	565	570
Asn Asn Thr Glu Asp Lys Leu Tyr Asn	Leu Leu Leu Leu Arg Met	
575	580	585
Cys Arg Tyr Val Lys Ile Ser Thr Glu	Thr Glu Glu Thr Glu Gly	
590	595	600
Ser Leu His Cys Cys Lys Asp Gln Asn	Ile Asn Gly Asn Gly Pro	
605	610	615
Asn Gly Ile His Glu Glu Gly Ser Pro	Ser Glu Met Glu Thr Asp	
620	625	630
Glu Pro Asp Asp Glu Ser Ser Gln Asp	Gln Glu Leu Pro Ser Glu	
635	640	645

Asn	Glu	Asn	Ser	Gln	Ser	Glu	Asp	Ser	Val	Gly	Gly	Asp	Asn	Asp	
				650					655					660	
Ser	Glu	Asn	Gly	Leu	Cys	Thr	Glu	Asp	Thr	Cys	Lys	Gly	Gln	Leu	
				665					670					675	
Thr	Gly	His	Lys	Lys	Arg	Leu	Phe	Thr	Phe	Gln	Phe	Asn	Asn	Leu	
				680					685					690	
Gly	Asn	Thr	Asp	Ile	Asn	Tyr	Ile	Lys	Asp	Asp	Thr	Arg	His	Ile	
				695					700					705	
Arg	Phe	Asp	Asp	Arg	Gln	Leu	Arg	Leu	Asp	Glu	Arg	Ser	Phe	Leu	
				710					715					720	
Ala	Leu	Asp	Trp	Asp	Pro	Asp	Leu	Lys	Lys	Arg	Tyr	Phe	Asp	Glu	
				725					730					735	
Asn	Ala	Ala	Glu	Asp	Phe	Glu	Lys	His	Glu	Ser	Val	Glu	Tyr	Lys	
				740					745					750	
Pro	Pro	Lys	Lys	Pro	Phe	Val	Lys	Leu	Lys	Asp	Cys	Ile	Glu	Leu	
				755					760					765	
Phe	Thr	Thr	Lys	Glu	Lys	Leu	Gly	Ala	Glu	Asp	Pro	Trp	Tyr	Cys	
				770					775					780	
Pro	Asn	Cys	Lys	Glu	His	Gln	Gln	Ala	Thr	Lys	Lys	Leu	Asp	Leu	
				785					790					795	
Trp	Ser	Leu	Pro	Pro	Val	Leu	Val	Val	His	Leu	Lys	Arg	Phe	Ser	
				800					805					810	
Tyr	Ser	Arg	Tyr	Met	Arg	Asp	Lys	Leu	Asp	Thr	Leu	Val	Asp	Phe	
				815					820					825	
Pro	Ile	Asn	Asp	Leu	Asp	Met	Ser	Glu	Phe	Leu	Ile	Asn	Pro	Asn	
				830					835					840	
Ala	Gly	Pro	Cys	Arg	Tyr	Asn	Leu	Ile	Ala	Val	Ser	Asn	His	Tyr	
				845					850					855	
Gly	Gly	Met	Gly	Gly	Gly	His	Tyr	Thr	Ala	Phe	Ala	Lys	Asn	Lys	
				860					865					870	
Asp	Asp	Gly	Lys	Trp	Tyr	Tyr	Phe	Asp	Asp	Ser	Ser	Val	Ser	Thr	
				875					880					885	
Ala	Ser	Glu	Asp	Gln	Ile	Val	Ser	Lys	Ala	Ala	Tyr	Val	Leu	Phe	
				890					895					900	
Tyr	Gln	Arg	Gln	Asp	Thr	Phe	Ser	Gly	Thr	Gly	Phe	Phe	Pro	Leu	
				905					910					915	
Asp	Arg	Glu	Thr	Lys	Gly	Ala	Ser	Ala	Ala	Thr	Gly	Ile	Pro	Leu	
				920					925					930	
Glu	Ser	Asp	Glu	Asp	Ser	Asn	Asp	Asn	Asp	Asn	Asp	Ile	Glu	Asn	
				935					940					945	
Glu	Asn	Cys	Met	His	Thr	Asn									
				950											

<210> 9

<211> 166

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 998626

<400> 9

Met	Leu	His	Pro	Glu	Thr	Ser	Pro	Gly	Arg	Gly	His	Leu	Leu	Ala	
1				5				10						15	
Val	Leu	Leu	Ala	Leu	Leu	Gly	Thr	Ala	Trp	Ala	Glu	Val	Trp	Pro	

20	25	30
Pro Gln Leu Gln Glu Gln Ala Pro Met Ala Gly Ala Leu Asn Arg		
35	40	45
Lys Glu Ser Phe Leu Leu Leu Ser Leu His Asn Arg Leu Arg Ser		
50	55	60
Trp Val Gln Pro Pro Ala Ala Asp Met Arg Arg Leu Asp Trp Ser		
65	70	75
Asp Ser Leu Ala Gln Leu Ala Gln Ala Arg Ala Ala Leu Cys Gly		
80	85	90
Ile Pro Thr Pro Ser Leu Ala Ser Gly Leu Trp Arg Thr Leu Gln		
95	100	105
Val Gly Trp Asn Met Gln Leu Leu Pro Ala Gly Leu Ala Ser Phe		
110	115	120
Val Glu Val Val Ser Leu Trp Phe Ala Glu Gly Gln Arg Tyr Ser		
125	130	135
His Ala Ala Gly Glu Cys Ala Arg Asn Ala Thr Cys Thr His Tyr		
140	145	150
Thr Gln Leu Val Trp Ala Thr Ser Ser Gln Leu Gly Cys Gly Arg		
155	160	165
His		

<210> 10

<211> 543

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 1393301

<400> 10

Met Arg Lys Pro Ala Ala Gly Phe Leu Pro Ser Leu Leu Lys Val		
1	5	10
Leu Leu Leu Pro Leu Ala Pro Ala Ala Gln Asp Ser Thr Gln		
20	25	30
Ala Ser Thr Pro Gly Ser Pro Leu Ser Pro Thr Glu Tyr Glu Arg		
35	40	45
Phe Phe Ala Leu Leu Thr Pro Thr Trp Lys Ala Glu Thr Thr Cys		
50	55	60
Arg Leu Arg Ala Thr His Gly Cys Arg Asn Pro Thr Leu Val Gln		
65	70	75
Leu Asp Gln Tyr Glu Asn His Gly Leu Val Pro Asp Gly Ala Val		
80	85	90
Cys Ser Asn Leu Pro Tyr Ala Ser Trp Phe Glu Ser Phe Cys Gln		
95	100	105
Phe Thr His Tyr Arg Cys Ser Asn His Val Tyr Tyr Ala Lys Arg		
110	115	120
Val Leu Cys Ser Gln Pro Val Ser Ile Leu Ser Pro Asn Thr Leu		
125	130	135
Lys Glu Ile Glu Ala Ser Ala Glu Val Ser Pro Thr Thr Met Thr		
140	145	150
Ser Pro Ile Ser Pro His Phe Thr Val Thr Glu Arg Gln Thr Phe		
155	160	165
Gln Pro Trp Pro Glu Arg Leu Ser Asn Asn Val Glu Glu Leu Leu		
170	175	180
Gln Ser Ser Leu Ser Leu Gly Gly Gln Glu Gln Ala Pro Glu His		

	185		190		195
Lys Gln Glu Gln Gly Val Glu His Arg		Gln Glu Pro Thr Gln Glu			
	200		205		210
His Lys Gln Glu Glu Gly Gln Lys Gln		Glu Glu Gln Glu Glu Glu			
	215		220		225
Gln Glu Glu Glu Gly Lys Gln Glu Glu		Gly Gln Gly Thr Lys Glu			
	230		235		240
Gly Arg Glu Ala Val Ser Gln Leu Gln		Thr Asp Ser Glu Pro Lys			
	245		250		255
Phe His Ser Glu Ser Leu Ser Ser Asn		Pro Ser Ser Phe Ala Pro			
	260		265		270
Arg Val Arg Glu Val Glu Ser Thr Pro		Met Ile Met Glu Asn Ile			
	275		280		285
Gln Glu Leu Ile Arg Ser Ala Gln Glu		Ile Asp Glu Met Asn Glu			
	290		295		300
Ile Tyr Asp Glu Asn Ser Tyr Trp Arg		Asn Gln Asn Pro Gly Ser			
	305		310		315
Leu Leu Gln Leu Pro His Thr Glu Ala		Leu Leu Val Leu Cys Tyr			
	320		325		330
Ser Ile Val Glu Asn Thr Cys Ile Ile		Thr Pro Thr Ala Lys Ala			
	335		340		345
Trp Lys Tyr Met Glu Glu Glu Ile Leu		Gly Phe Gly Lys Ser Val			
	350		355		360
Cys Asp Ser Leu Gly Arg Arg His Met		Ser Thr Cys Ala Leu Cys			
	365		370		375
Asp Phe Cys Ser Leu Lys Leu Glu Gln		Cys His Ser Glu Ala Ser			
	380		385		390
Leu Gln Arg Gln Gln Cys Asp Thr Ser		His Lys Thr Pro Phe Val			
	395		400		405
Ser Pro Leu Leu Ala Ser Gln Ser Leu		Ser Ile Gly Asn Gln Val			
	410		415		420
Gly Ser Pro Glu Ser Gly Arg Phe Tyr		Gly Leu Asp Leu Tyr Gly			
	425		430		435
Gly Leu His Met Asp Phe Trp Cys Ala		Arg Leu Ala Thr Lys Gly			
	440		445		450
Cys Glu Asp Val Arg Val Ser Gly Trp		Leu Gln Thr Glu Phe Leu			
	455		460		465
Ser Phe Gln Asp Gly Asp Phe Pro Thr		Lys Ile Cys Asp Thr Asp			
	470		475		480
Tyr Ile Gln Tyr Pro Asn Tyr Cys Ser		Phe Lys Ser Gln Gln Cys			
	485		490		495
Leu Met Arg Asn Arg Asn Arg Lys Val		Ser Arg Met Arg Cys Leu			
	500		505		510
Gln Asn Glu Thr Tyr Ser Ala Leu Ser		Pro Gly Lys Ser Glu Asp			
	515		520		525
Val Val Leu Arg Trp Ser Gln Glu Phe		Ser Thr Leu Thr Leu Gly			
	530		535		540
Gln Phe Gly					

<210> 11
 <211> 83
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature

<223> Incyte Clone No: 1444055

<400> 11

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Met Ile Gly Trp Asp Ser Leu Arg Leu Ile Leu Gly Asn Thr Asp
 1           5           10           15
Asn Val Ser Arg Arg Asp Ser Thr Arg Gly Ser Ile Phe Ile Thr
          20           25           30
Gln Leu Ile Ala Cys Phe Gln Arg Tyr Ser Trp Arg Cys His Leu
          35           40           45
Glu Glu Val Phe Trp Lys Val Gln Gln Ala Phe Glu Ser Pro Glu
          50           55           60
Ala Thr Val Gln Met Pro Thr Ile Glu Arg Val Ser Met Thr Arg
          65           70           75
Tyr Phe Tyr Leu Phe Pro Gly Asn
          80

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<210> 12

<211> 648

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 1650177

<400> 12

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Met Leu Gly Ser Leu Val Leu Arg Arg Lys Ala Leu Ala Pro Arg
 1           5           10           15
Leu Leu Leu Arg Leu Leu Arg Ser Pro Thr Leu Arg Gly His Gly
          20           25           30
Gly Ala Ser Gly Arg Asn Val Thr Thr Gly Ser Leu Gly Glu Pro
          35           40           45
Gln Trp Leu Arg Val Ala Thr Gly Gly Arg Pro Gly Thr Ser Pro
          50           55           60
Ala Leu Phe Ser Gly Arg Gly Ala Ala Thr Gly Gly Arg Gln Gly
          65           70           75
Gly Arg Phe Asp Thr Lys Cys Leu Ala Ala Ala Thr Trp Gly Arg
          80           85           90
Leu Pro Gly Pro Glu Glu Thr Leu Pro Gly Gln Asp Ser Trp Asn
          95          100          105
Gly Val Pro Ser Arg Ala Gly Leu Gly Met Cys Ala Leu Ala Ala
          110          115          120
Ala Leu Val Val His Cys Tyr Ser Lys Ser Pro Ser Asn Lys Asp
          125          130          135
Ala Ala Leu Leu Glu Ala Ala Arg Ala Asn Asn Met Gln Glu Val
          140          145          150
Ser Ser Val Val Gln Val Leu Leu Ala Ala Gly Ala Asp Pro Asn
          155          160          165
Leu Gly Asp Asp Phe Ser Ser Val Phe Lys Thr Ala Lys Glu Gln
          170          175          180
Gly Ile His Ser Leu Glu Val Leu Ile Thr Arg Glu Asp Asp Phe
          185          190          195
Asn Asn Arg Leu Asn Asn Arg Ala Ser Phe Lys Gly Cys Thr Ala
          200          205          210
Leu His Tyr Ala Val Leu Ala Asp Asp Tyr Arg Thr Val Lys Glu
          215          220          225

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Leu Leu Asp Gly Gly Ala Asn Pro Leu Gln Arg Asn Glu Met Gly	230	235	240
His Thr Pro Leu Asp Tyr Ala Arg Glu Gly Glu Val Met Lys Leu	245	250	255
Leu Arg Thr Ser Glu Ala Lys Tyr Gln Glu Lys Gln Arg Lys Arg	260	265	270
Glu Ala Glu Glu Arg Arg Arg Phe Pro Leu Glu Gln Arg Leu Lys	275	280	285
Glu His Ile Ile Gly Gln Glu Ser Ala Ile Ala Thr Val Gly Ala	290	295	300
Ala Ile Arg Arg Lys Glu Asn Gly Trp Tyr Asp Glu Glu His Pro	305	310	315
Leu Val Phe Leu Phe Leu Gly Ser Ser Gly Ile Gly Lys Thr Glu	320	325	330
Leu Ala Lys Gln Thr Ala Lys Tyr Met His Lys Asp Ala Lys Lys	335	340	345
Gly Phe Ile Arg Leu Asp Met Ser Glu Phe Gln Glu Arg His Glu	350	355	360
Val Ala Lys Phe Ile Gly Ser Pro Pro Gly Tyr Val Gly His Glu	365	370	375
Glu Gly Gly Gln Leu Thr Lys Lys Leu Lys Gln Cys Pro Asn Ala	380	385	390
Val Val Leu Phe Asp Glu Val Asp Lys Ala His Pro Asp Val Leu	395	400	405
Thr Ile Met Leu Gln Leu Phe Asp Glu Gly Arg Leu Thr Asp Gly	410	415	420
Lys Gly Lys Thr Ile Asp Cys Lys Asp Ala Ile Phe Ile Met Thr	425	430	435
Ser Asn Val Ala Ser Asp Glu Ile Ala Gln His Ala Leu Gln Leu	440	445	450
Arg Gln Glu Ala Leu Glu Met Ser Arg Asn Arg Ile Ala Glu Asn	455	460	465
Leu Gly Asp Val Gln Ile Ser Asp Lys Ile Thr Ile Ser Lys Asn	470	475	480
Phe Lys Glu Asn Val Ile Arg Pro Ile Leu Lys Ala His Phe Arg	485	490	495
Arg Asp Glu Phe Leu Gly Arg Ile Asn Glu Ile Val Tyr Phe Leu	500	505	510
Pro Phe Cys His Ser Glu Leu Ile Gln Leu Val Asn Lys Glu Leu	515	520	525
Asn Phe Trp Ala Lys Arg Ala Lys Gln Arg His Asn Ile Thr Leu	530	535	540
Leu Trp Asp Arg Glu Val Ala Asp Val Leu Val Asp Gly Tyr Asn	545	550	555
Val His Tyr Gly Ala Arg Ser Ile Lys His Glu Val Glu Arg Arg	560	565	570
Val Val Asn Gln Leu Ala Ala Ala Tyr Glu Gln Asp Leu Leu Pro	575	580	585
Gly Gly Cys Thr Leu Arg Ile Thr Val Glu Asp Ser Asp Lys Gln	590	595	600
Leu Leu Lys Ser Pro Glu Leu Pro Ser Pro Gln Ala Glu Lys Arg	605	610	615
Leu Pro Lys Leu Arg Leu Glu Ile Ile Asp Lys Asp Ser Lys Thr	620	625	630
Arg Arg Leu Asp Ile Arg Ala Pro Leu His Pro Glu Lys Val Cys	635	640	645
Asn Thr Ile			

<210> 13
 <211> 672
 <212> PRT
 <213> Homo sapiens

<220>
 <221> misc_feature
 <223> Incyte Clone No: 1902576

<400> 13
 Met Arg Ala Gly Arg Gly Ala Thr Pro Ala Arg Glu Leu Phe Arg
 1 5 10 15
 Asp Ala Ala Phe Pro Ala Ala Asp Ser Ser Leu Phe Cys Asp Leu
 20 25 30
 Ser Thr Pro Leu Ala Gln Phe Arg Glu Asp Ile Thr Trp Arg Arg
 35 40 45
 Pro Gln Glu Ile Cys Ala Thr Pro Arg Leu Phe Pro Asp Asp Pro
 50 55 60
 Arg Glu Gly Gln Val Lys Gln Gly Leu Leu Gly Asp Cys Trp Phe
 65 70 75
 Leu Cys Ala Cys Ala Ala Leu Gln Lys Ser Arg His Leu Leu Asp
 80 85 90
 Gln Val Ile Pro Pro Gly Gln Pro Ser Trp Ala Asp Gln Glu Tyr
 95 100 105
 Arg Gly Ser Phe Thr Cys Arg Ile Trp Gln Phe Gly Arg Trp Val
 110 115 120
 Glu Val Thr Thr Asp Asp Arg Leu Pro Cys Leu Ala Gly Arg Leu
 125 130 135
 Cys Phe Ser Arg Cys Gln Arg Glu Asp Val Phe Trp Leu Pro Leu
 140 145 150
 Leu Glu Lys Val Tyr Ala Lys Val His Gly Ser Tyr Glu His Leu
 155 160 165
 Trp Ala Gly Gln Val Ala Asp Ala Leu Val Asp Leu Thr Gly Gly
 170 175 180
 Leu Ala Glu Arg Trp Asn Leu Lys Gly Val Ala Gly Ser Gly Gly
 185 190 195
 Gln Gln Asp Arg Pro Gly Arg Trp Glu His Arg Thr Cys Arg Gln
 200 205 210
 Leu Leu His Leu Lys Asp Gln Cys Leu Ile Ser Cys Cys Val Leu
 215 220 225
 Ser Pro Arg Ala Gly Ala Arg Glu Leu Gly Glu Phe His Ala Phe
 230 235 240
 Ile Val Ser Asp Leu Arg Glu Leu Gln Gly Gln Ala Gly Gln Cys
 245 250 255
 Ile Leu Leu Leu Arg Ile Gln Asn Pro Trp Gly Arg Arg Cys Trp
 260 265 270
 Gln Gly Leu Trp Arg Glu Gly Gly Glu Gly Trp Ser Gln Val Asp
 275 280 285
 Ala Ala Val Ala Ser Glu Leu Leu Ser Gln Leu Gln Glu Gly Glu
 290 295 300
 Phe Trp Val Glu Glu Glu Phe Leu Arg Glu Phe Asp Glu Leu
 305 310 315
 Thr Val Gly Tyr Pro Val Thr Glu Ala Gly His Leu Gln Ser Leu
 320 325 330
 Tyr Thr Glu Arg Leu Leu Cys His Thr Arg Ala Leu Pro Gly Ala
 335 340 345

Trp Val Lys Gly Gln Ser Ala Gly Gly Cys Arg Asn Asn Ser Gly
 350 355 360
 Phe Pro Ser Asn Pro Lys Phe Trp Leu Arg Val Ser Glu Pro Ser
 365 370 375
 Glu Val Tyr Ile Ala Val Leu Gln Arg Ser Arg Leu His Ala Ala
 380 385 390
 Asp Trp Ala Gly Arg Ala Arg Ala Leu Val Gly Asp Ser His Thr
 395 400 405
 Ser Trp Ser Pro Ala Ser Ile Pro Gly Lys His Tyr Gln Ala Val
 410 415 420
 Gly Leu His Leu Trp Lys Val Glu Lys Arg Arg Val Asn Leu Pro
 425 430 435
 Arg Val Leu Ser Met Pro Pro Val Ala Gly Thr Ala Cys His Ala
 440 445 450
 Tyr Asp Arg Glu Val His Leu Arg Cys Glu Leu Ser Pro Gly Tyr
 455 460 465
 Tyr Leu Ala Val Pro Ser Thr Phe Leu Lys Asp Ala Pro Gly Glu
 470 475 480
 Phe Leu Leu Arg Val Phe Ser Thr Gly Arg Val Ser Leu Ser Ala
 485 490 495
 Ile Arg Ala Val Ala Lys Asn Thr Ala Pro Gly Ala Ala Leu Pro
 500 505 510
 Ala Gly Glu Trp Gly Thr Val Gln Leu Arg Gly Ser Trp Arg Val
 515 520 525
 Gly Gln Thr Ala Gly Gly Ser Arg Asn Phe Ala Ser Tyr Pro Thr
 530 535 540
 Asn Pro Cys Phe Pro Phe Ser Val Pro Glu Gly Pro Gly Pro Arg
 545 550 555
 Cys Val Arg Ile Thr Leu His Gln His Cys Arg Pro Ser Asp Thr
 560 565 570
 Glu Phe His Pro Ile Gly Phe His Ile Phe Gln Val Pro Glu Gly
 575 580 585
 Gly Arg Ser Gln Asp Ala Pro Pro Leu Leu Leu Gln Glu Pro Leu
 590 595 600
 Leu Ser Cys Val Pro His Arg Tyr Ala Gln Glu Val Ser Arg Leu
 605 610 615
 Cys Leu Leu Pro Ala Gly Thr Tyr Lys Val Val Pro Ser Thr Tyr
 620 625 630
 Leu Pro Asp Thr Glu Gly Ala Phe Thr Val Thr Ile Ala Thr Arg
 635 640 645
 Ile Asp Arg Pro Ser Ile His Ser Gln Glu Met Leu Gly Gln Phe
 650 655 660
 Leu Gln Glu Val Ser Val Met Ala Val Met Lys Thr
 665 670

<210> 14

<211> 80

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 2024210

<400> 14

Met Lys Leu Ser Gly Met Phe Leu Leu Leu Ser Leu Ala Leu Phe

1	5	10	15
Cys Phe Leu Thr Gly Val Phe Ser Gln Gly Gly Gln Val Asp Cys			
	20	25	30
Gly Glu Phe Gln Asp Pro Lys Val Tyr Cys Thr Arg Glu Ser Asn			
	35	40	45
Pro His Cys Gly Ser Asp Gly Gln Thr Tyr Gly Asn Lys Cys Ala			
	50	55	60
Phe Cys Lys Ala Ile Val Lys Ser Gly Gly Lys Ile Ser Leu Lys			
	65	70	75
His Pro Gly Lys Cys			
	80		

<210> 15

<211> 795

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 2523109

<400> 15

Met Ala Val Leu Leu Leu Leu Arg Ala Leu Arg Arg Gly Pro		
1	5	10
Gly Pro Gly Pro Arg Pro Leu Trp Gly Pro Gly Pro Ala Trp Ser		
	20	25
Pro Gly Phe Pro Ala Arg Pro Gly Arg Gly Arg Pro Tyr Met Ala		
	35	40
Ser Arg Pro Pro Gly Asp Leu Ala Glu Ala Gly Gly Arg Ala Leu		
	50	55
Gln Ser Leu Gln Leu Arg Leu Leu Thr Pro Thr Phe Glu Gly Ile		
	65	70
Asn Gly Leu Leu Leu Lys Gln His Leu Val Gln Asn Pro Val Arg		
	80	85
Leu Trp Gln Leu Leu Gly Gly Thr Phe Tyr Phe Asn Thr Ser Arg		
	95	100
Leu Lys Gln Lys Asn Lys Glu Lys Asp Lys Ser Lys Gly Lys Ala		
	110	115
Pro Glu Glu Asp Glu Glu Glu Arg Arg Arg Arg Glu Arg Asp Asp		
	125	130
Gln Met Tyr Arg Glu Arg Leu Arg Thr Leu Leu Val Ile Ala Val		
	140	145
Val Met Ser Leu Leu Asn Ala Leu Ser Thr Ser Gly Gly Ser Ile		
	155	160
Ser Trp Asn Asp Phe Val His Glu Met Leu Ala Lys Gly Glu Val		
	170	175
Gln Arg Val Gln Val Val Pro Glu Ser Asp Val Val Glu Val Tyr		
	185	190
Leu His Pro Gly Ala Val Val Phe Gly Arg Pro Arg Leu Ala Leu		
	200	205
Met Tyr Arg Met Gln Val Ala Asn Ile Asp Lys Phe Glu Glu Lys		
	215	220
Leu Arg Ala Ala Glu Asp Glu Leu Asn Ile Glu Ala Lys Asp Arg		
	230	235
Ile Pro Val Ser Tyr Lys Arg Thr Gly Phe Phe Gly Asn Ala Leu		
	245	250
		255

Tyr Ser Val Gly Met Thr Ala Val Gly Leu Ala Ile Leu Trp Tyr		
	260	265
Val Phe Arg Leu Ala Gly Met Thr Gly Arg Glu Gly Gly Phe Ser		270
	275	280
Ala Phe Asn Gln Leu Lys Met Ala Arg Phe Thr Ile Val Asp Gly		285
	290	295
Lys Met Gly Lys Gly Val Ser Phe Lys Asp Val Ala Gly Met His		300
	305	310
Glu Ala Lys Leu Glu Val Arg Glu Phe Val Asp Tyr Leu Lys Ser		315
	320	325
Pro Lys Arg Phe Leu Gln Leu Gly Ala Lys Val Pro Lys Gly Ala		330
	335	340
Leu Leu Leu Gly Pro Pro Gly Cys Gly Lys Thr Leu Leu Ala Lys		345
	350	355
Ala Val Ala Thr Glu Ala Gln Val Pro Phe Leu Ala Met Ala Gly		360
	365	370
Pro Glu Phe Val Glu Val Ile Gly Gly Leu Gly Ala Ala Arg Val		375
	380	385
Arg Ser Leu Phe Lys Glu Ala Arg Ala Arg Ala Pro Cys Ile Val		390
	395	400
Tyr Ile Asp Glu Ile Asp Ala Val Gly Lys Lys Arg Ser Thr Thr		405
	410	415
Met Ser Gly Phe Ser Asn Thr Glu Glu Glu Gln Thr Leu Asn Gln		420
	425	430
Leu Leu Val Glu Met Asp Gly Met Gly Thr Thr Asp His Val Ile		435
	440	445
Val Leu Ala Ser Thr Asn Arg Ala Asp Ile Leu Asp Gly Ala Leu		450
	455	460
Met Arg Pro Gly Arg Leu Asp Arg His Val Phe Ile Asp Leu Pro		465
	470	475
Thr Leu Gln Glu Arg Arg Glu Ile Phe Glu Gln His Leu Lys Ser		480
	485	490
Leu Lys Leu Thr Gln Ser Ser Thr Phe Tyr Ser Gln Arg Leu Ala		495
	500	505
Glu Leu Thr Pro Gly Phe Ser Gly Ala Asp Ile Ala Asn Ile Cys		510
	515	520
Asn Glu Ala Ala Leu His Ala Ala Arg Glu Gly His Thr Ser Val		525
	530	535
His Thr Leu Asn Phe Glu Tyr Ala Val Glu Arg Val Leu Ala Gly		540
	545	550
Thr Ala Lys Lys Ser Lys Ile Leu Ser Lys Glu Glu Gln Lys Val		555
	560	565
Val Ala Phe His Glu Ser Gly His Ala Leu Val Gly Trp Met Leu		570
	575	580
Glu His Thr Glu Ala Val Met Lys Val Ser Ile Thr Pro Arg Thr		585
	590	595
Asn Ala Ala Leu Gly Phe Ala Gln Met Leu Pro Arg Asp Gln His		600
	605	610
Leu Phe Thr Lys Glu Gln Leu Phe Glu Arg Met Cys Met Ala Leu		615
	620	625
Gly Gly Arg Ala Ser Glu Ala Leu Ser Phe Asn Glu Val Thr Ser		630
	635	640
Gly Ala Gln Asp Asp Leu Arg Lys Val Thr Arg Ile Ala Tyr Ser		645
	650	655
Met Val Lys Gln Phe Gly Met Ala Pro Gly Ile Gly Pro Ile Ser		660
	665	670
Phe Pro Glu Ala Gln Glu Gly Leu Met Gly Ile Gly Arg Arg Pro		675

680	685	690
Phe Ser Gln Gly Leu Gln Gln Met Met Asp His Glu Ala Arg Leu		
695	700	705
Leu Val Ala Lys Ala Tyr Arg His Thr Glu Lys Val Leu Gln Asp		
710	715	720
Asn Leu Asp Lys Leu Gln Ala Leu Ala Asn Ala Leu Leu Glu Lys		
725	730	735
Glu Val Ile Asn Tyr Glu Asp Ile Glu Ala Leu Ile Gly Pro Pro		
740	745	750
Pro His Gly Pro Lys Lys Met Ile Ala Pro Gln Arg Trp Ile Asp		
755	760	765
Ala Gln Arg Glu Lys Gln Asp Leu Gly Glu Glu Glu Thr Glu Glu		
770	775	780
Thr Gln Gln Pro Pro Leu Gly Gly Glu Glu Pro Thr Trp Pro Lys		
785	790	795

<210> 16

<211> 193

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 2588566

<400> 16

Met Pro Asp Ser Asp Arg His Leu Ser Ser His Phe Asn Leu Arg	
1 5 10 15	
Met Lys Gly Ser Pro Ser Glu His Gly Ser Gln Gln Ser Ile Phe	
20 25 30	
Asn Arg Tyr Ala Gln Gln Arg Leu Asp Ile Asp Ala Thr Gln Leu	
35 40 45	
Gln Gly Leu Leu Asn Gln Glu Leu Leu Thr Gly Pro Pro Gly Asp	
50 55 60	
Met Phe Ser Leu Asp Glu Cys Arg Ser Leu Val Ala Leu Met Glu	
65 70 75	
Leu Lys Val Asn Gly Arg Leu Asp Gln Glu Glu Phe Ala Arg Leu	
80 85 90	
Trp Lys Arg Leu Val His Tyr Gln His Val Phe Gln Lys Val Gln	
95 100 105	
Thr Ser Pro Gly Val Leu Leu Ser Ser Asp Leu Trp Lys Ala Ile	
110 115 120	
Glu Asn Thr Asp Phe Leu Arg Gly Ile Phe Ile Ser Arg Glu Leu	
125 130 135	
Leu His Leu Val Thr Leu Arg Tyr Ser Asp Ser Val Gly Arg Val	
140 145 150	
Ser Phe Pro Ser Leu Val Cys Phe Leu Met Arg Leu Glu Ala Met	
155 160 165	
Ala Lys Thr Phe Arg Asn Leu Ser Lys Asp Gly Lys Gly Leu Tyr	
170 175 180	
Leu Thr Glu Met Glu Trp Met Ser Leu Val Met Tyr Asn	
185 190	

<210> 17

<211> 663

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 2740570

<400> 17

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Met Asp Leu Leu His Glu Glu Leu Lys Glu Gln Val Met Glu Val
 1          5          10          15
Glu Glu Asp Pro Gln Thr Ile Thr Thr Glu Glu Thr Met Glu Glu
          20          25          30
Asp Lys Ser Gln Ser Asp Val Asp Phe Gln Ser Cys Glu Ser Cys
          35          40          45
Ser Asn Ser Asp Arg Ala Glu Asn Glu Asn Gly Ser Arg Cys Phe
          50          55          60
Ser Glu Asp Asn Asn Glu Thr Thr Met Leu Ile Gln Asp Asp Glu
          65          70          75
Asn Asn Ser Glu Met Ser Lys Asp Trp Gln Lys Glu Lys Met Cys
          80          85          90
Asn Lys Ile Asn Lys Val Asn Ser Glu Gly Glu Phe Asp Lys Asp
          95          100          105
Arg Asp Ser Ile Ser Glu Thr Val Asp Leu Asn Asn Gln Glu Thr
          110          115          120
Val Lys Val Gln Ile His Ser Arg Ala Ser Glu Tyr Ile Thr Asp
          125          130          135
Val His Ser Asn Asp Leu Ser Thr Pro Gln Ile Leu Pro Ser Asn
          140          145          150
Glu Gly Val Asn Pro Arg Leu Ser Ala Ser Pro Pro Lys Ser Gly
          155          160          165
Asn Leu Trp Pro Gly Leu Ala Pro Pro His Lys Lys Ala Gln Ser
          170          175          180
Ala Ser Pro Lys Arg Lys Lys Gln His Lys Lys Tyr Arg Ser Val
          185          190          195
Ile Ser Asp Ile Phe Asp Gly Thr Ile Ile Ser Ser Val Gln Cys
          200          205          210
Leu Thr Cys Asp Arg Val Ser Val Thr Leu Glu Thr Phe Gln Asp
          215          220          225
Leu Ser Leu Pro Ile Pro Gly Lys Glu Asp Leu Ala Lys Leu His
          230          235          240
Ser Ser Ser His Pro Thr Ser Ile Val Lys Ala Gly Ser Cys Gly
          245          250          255
Glu Ala Tyr Ala Pro Gln Gly Trp Ile Ala Phe Phe Met Glu Tyr
          260          265          270
Val Lys Arg Phe Val Val Ser Cys Val Pro Ser Trp Phe Trp Gly
          275          280          285
Pro Val Val Thr Leu Gln Asp Cys Leu Ala Ala Phe Phe Ala Arg
          290          295          300
Asp Glu Leu Lys Gly Asp Asn Met Tyr Ser Cys Glu Lys Cys Lys
          305          310          315
Lys Leu Arg Asn Gly Val Lys Phe Cys Lys Val Gln Asn Phe Pro
          320          325          330
Glu Ile Leu Cys Ile His Leu Lys Arg Phe Arg His Glu Leu Met
          335          340          345
Phe Ser Thr Lys Ile Ser Thr His Val Ser Phe Pro Leu Glu Gly
          350          355          360
Leu Asp Leu Gln Pro Phe Leu Ala Lys Asp Ser Pro Ala Gln Ile

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365	370	375
Val Thr Tyr Asp Leu Leu Ser Val Ile Cys His His Gly Thr Ala		
380	385	390
Ser Ser Gly His Tyr Ile Ala Tyr Cys Arg Asn Asn Leu Asn Asn		
395	400	405
Leu Trp Tyr Glu Phe Asp Asp Gln Ser Val Thr Glu Val Ser Glu		
410	415	420
Ser Thr Val Gln Asn Ala Glu Ala Tyr Val Leu Phe Tyr Arg Lys		
425	430	435
Ser Ser Glu Glu Ala Gln Lys Glu Arg Arg Arg Ile Ser Asn Leu		
440	445	450
Leu Asn Ile Met Glu Pro Ser Leu Leu Gln Phe Tyr Ile Ser Arg		
455	460	465
Gln Trp Leu Asn Lys Phe Lys Thr Phe Ala Glu Pro Gly Pro Ile		
470	475	480
Ser Asn Asn Asp Phe Leu Cys Ile His Gly Gly Val Pro Pro Arg		
485	490	495
Lys Ala Gly Tyr Ile Glu Asp Leu Val Leu Met Leu Pro Gln Asn		
500	505	510
Ile Trp Asp Asn Leu Tyr Ser Arg Tyr Gly Gly Gly Pro Ala Val		
515	520	525
Asn His Leu Tyr Ile Cys His Thr Cys Gln Ile Glu Ala Glu Lys		
530	535	540
Ile Glu Lys Arg Arg Lys Thr Glu Leu Glu Ile Phe Ile Arg Leu		
545	550	555
Asn Arg Ala Phe Gln Lys Glu Asp Ser Pro Ala Thr Phe Tyr Cys		
560	565	570
Ile Ser Met Gln Trp Phe Arg Glu Trp Glu Ser Phe Val Lys Gly		
575	580	585
Lys Asp Gly Asp Pro Pro Gly Pro Ile Asp Asn Thr Lys Ile Ala		
590	595	600
Val Thr Lys Cys Gly Asn Val Met Leu Arg Gln Gly Ala Asp Ser		
605	610	615
Gly Gln Ile Ser Glu Glu Thr Trp Asn Phe Leu Gln Ser Ile Tyr		
620	625	630
Gly Gly Gly Pro Glu Val Ile Leu Arg Pro Pro Val Val His Val		
635	640	645
Asp Pro Asp Ile Leu Gln Ala Glu Glu Lys Ile Glu Val Glu Thr		
650	655	660
Arg Ser Leu		

<210> 18

<211> 362

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 2820384

<400> 18

Met Tyr Ser Cys Glu Arg Cys Lys Lys Leu Arg Asn Gly Val Lys		
1	5	10
		15
Tyr Cys Lys Val Leu Arg Leu Pro Glu Ile Leu Cys Ile His Leu		
20	25	30
Lys Arg Phe Arg His Glu Val Met Tyr Ser Phe Lys Ile Asn Ser		

	35	40	45
His Val Ser Phe Pro Leu Glu Gly Leu Asp Leu Arg Pro Phe Leu			
	50	55	60
Ala Lys Glu Cys Thr Ser Gln Ile Thr Thr Tyr Asp Leu Leu Ser			
	65	70	75
Val Ile Cys His His Gly Thr Ala Gly Ser Gly His Tyr Ile Ala			
	80	85	90
Tyr Cys Gln Asn Val Ile Asn Gly Gln Trp Tyr Glu Phe Asp Asp			
	95	100	105
Gln Tyr Val Thr Glu Val His Glu Thr Val Val Gln Asn Ala Glu			
	110	115	120
Gly Tyr Val Leu Phe Tyr Arg Lys Ser Ser Glu Glu Ala Met Arg			
	125	130	135
Glu Arg Gln Gln Val Val Ser Leu Ala Ala Met Arg Glu Pro Ser			
	140	145	150
Leu Leu Arg Phe Tyr Val Ser Arg Glu Trp Leu Asn Lys Phe Asn			
	155	160	165
Thr Phe Ala Glu Pro Gly Pro Ile Thr Asn Gln Thr Phe Leu Cys			
	170	175	180
Ser His Gly Gly Ile Pro Pro His Lys Tyr His Tyr Ile Asp Asp			
	185	190	195
Leu Val Val Ile Leu Pro Gln Asn Val Trp Glu His Leu Tyr Asn			
	200	205	210
Arg Phe Gly Gly Gly Pro Ala Val Asn His Leu Tyr Val Cys Ser			
	215	220	225
Ile Cys Gln Val Glu Ile Glu Ala Leu Ala Lys Arg Arg Arg Ile			
	230	235	240
Glu Ile Asp Thr Phe Ile Lys Leu Asn Lys Ala Phe Gln Ala Glu			
	245	250	255
Glu Ser Pro Gly Val Ile Tyr Cys Ile Ser Met Gln Trp Phe Arg			
	260	265	270
Glu Trp Glu Ala Phe Val Lys Gly Lys Asp Asn Glu Pro Pro Gly			
	275	280	285
Pro Ile Asp Asn Ser Arg Ile Ala Gln Val Lys Gly Ser Gly His			
	290	295	300
Val Gln Leu Lys Gln Gly Ala Asp Tyr Gly Gln Ile Ser Glu Glu			
	305	310	315
Thr Trp Thr Tyr Leu Asn Ser Leu Tyr Gly Gly Gly Pro Glu Ile			
	320	325	330
Ala Ile Arg Gln Ser Val Ala Gln Arg Trp Ala Gln Arg Thr Cys			
	335	340	345
Thr Gly Ser Arg Arg Ser Lys Pro Arg Arg Gly Pro Cys Asp Leu			
	350	355	360
Leu Gly			

<210> 19

<211> 210

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 2990692

<400> 19

Met Val Ser Leu Leu Pro Gly Glu Pro Pro Gln Lys Ile Pro Arg

1	5	10	15
Gly Val Tyr Gly	Pro Leu Pro Glu Gly	Arg Val Gly Leu Ile Leu	
	20	25	30
Gly Arg Ser Ser	Leu Asn Leu Lys Gly Val Gln Ile His Thr Gly		
	35	40	45
Val Ile Tyr Ser	Asp Tyr Lys Gly Gly Ile Gln Leu Val Ile Ser		
	50	55	60
Ser Thr Val Pro	Trp Ser Ala Asn Pro Gly Asp Arg Ile Ala Gln		
	65	70	75
Leu Leu Leu Leu	Pro Tyr Val Lys Ile Gly Glu Asn Lys Thr Glu		
	80	85	90
Arg Thr Gly Gly	Phe Gly Ser Thr Asn Pro Ala Gly Lys Ala Thr		
	95	100	105
Tyr Trp Ala Asn	Gln Val Ser Glu Asp Arg Pro Val Cys Thr Val		
	110	115	120
Thr Ile Pro Gly	Lys Glu Phe Glu Gly Leu Val Asp Thr Gln Ala		
	125	130	135
Asp Val Ser Ile	Ile Gly Ile Gly Thr Ala Ser Glu Val Tyr Gln		
	140	145	150
Ser Ala Met Ile	Leu His Cys Leu Gly Ser Asp Asn Gln Glu Ser		
	155	160	165
Thr Val Gln Pro	Met Ile Thr Ser Ile Pro Ile Asn Leu Trp Gly		
	170	175	180
Arg Asp Leu Leu	Gln Trp His Ala Glu Ile Thr Ile Pro Ala		
	185	190	195
Ser Leu Tyr Ser	Pro Arg Asn Gln Lys Ile Met Thr Lys Met Gly		
	200	205	210

<210> 20

<211> 283

<212> PRT

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 4590384

<400> 20

Met Gly Leu Gly	Leu Arg Gly Trp Gly	Arg Pro Leu Leu Thr Val
1	5	10
Ala Thr Ala Leu	Met Leu Pro Val Lys Pro	Pro Ala Gly Ser Trp
	20	25
Gly Ala Gln Ile	Ile Gly Gly His Glu Val Thr	Pro His Ser Arg
	35	40
Pro Tyr Met Ala	Ser Val Arg Phe Gly Gly	Gln His His Cys Gly
	50	55
Gly Phe Leu Leu	Arg Ala Arg Trp Val Val	Ser Ala Ala His Cys
	65	70
Phe Ser His Arg	Asp Leu Arg Thr Gly Leu	Val Val Leu Gly Ala
	80	85
His Val Leu Ser	Thr Ala Glu Pro Thr Gln	Gln Val Phe Gly Ile
	95	100
Asp Ala Leu Thr	Thr His Pro Asp Tyr His	Pro Met Thr His Ala
	110	115
Asn Asp Ile Cys	Leu Leu Arg Leu Asn Gly	Ser Ala Val Leu Gly
	125	130
		135

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Pro Ala Val Gly Leu Leu Arg Leu Pro Gly Arg Arg Ala Arg Pro
      140                      145                      150
Pro Thr Ala Gly Thr Arg Cys Arg Val Ala Gly Trp Gly Phe Val
      155                      160                      165
Ser Asp Phe Glu Glu Leu Pro Pro Gly Leu Met Glu Ala Lys Val
      170                      175                      180
Arg Val Leu Asp Pro Asp Val Cys Asn Ser Ser Trp Lys Gly His
      185                      190                      195
Leu Thr Leu Thr Met Leu Cys Thr Arg Ser Gly Asp Ser His Arg
      200                      205                      210
Arg Gly Phe Cys Ser Ala Asp Ser Gly Gly Pro Leu Val Cys Arg
      215                      220                      225
Asn Arg Ala His Gly Leu Val Ser Phe Ser Gly Leu Trp Cys Gly
      230                      235                      240
Asp Pro Lys Thr Pro Asp Val Tyr Thr Gln Val Ser Ala Phe Val
      245                      250                      255
Ala Trp Ile Trp Asp Val Val Arg Arg Ser Ser Pro Gln Pro Gly
      260                      265                      270
Pro Leu Pro Gly Thr Thr Arg Pro Pro Gly Glu Ala Ala
      275                      280

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<210> 21

<211> 896

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 660

<223> a or g or c or t, unknown, or other

<220>

<221> misc_feature

<223> Incyte Clone No: 1220330

<400> 21

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gacgtgctgg gcgtggcggg gctggtcagg cggcgtcgtc ggtacgctct gacgggcagc 180
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catgccttct tccctgggga gcaccccatc tccggggaca ctactttga cgatgaggag 480
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<210> 22

<211> 4906

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 1342493

<400> 22

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gttgttgcca tggcattcgc cagctggtgg tacaagacgc atgtcagtga aaaaaccagt 180
gaatcgccctt ccaaaccagg agaaaagaaa ggatcagatg agaaaaaagc agcaagcctc 240
ggcagcagtc aatcctccag aacctatgct ggtggaacag cctcggccac caagggtgtca 300
gttctctctg gtgcaaccag caagtcttcc agtatgaatc ccacagaaac caaggctgtgta 360
aaaaacagaac ctgagaagaa gtcacagtca accaagctgt ctgtggttca tgagaaaaaa 420
tccaagaag gaaagccaaa agaacacaca gagccaaaaa gcctacccaa gcaggcatca 480
gatacaggaa gtaacgatgc tcacaataaa aaagcagttt ccagatcagc tgaacagcag 540
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<213> Homo sapiens

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<223> Incyte Clone No: 1698270

<400> 23

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<210> 24

<211> 849

<212> DNA

<213> Homo sapiens

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<221> misc_feature

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<210> 25

<211> 2166

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<223> Incyte Clone No: 2309875

<400> 25

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<210> 26

<211> 2069

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 2479394

<400> 26

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2069

<210> 27

<211> 2490

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 2613215

<400> 27

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<210> 28

<211> 3148

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 001528

<400> 28

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<210> 29

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<212> DNA

<213> Homo sapiens

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<220>

<221> misc_feature

<223> Incyte Clone No: 998626

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<211> 1912

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<223> Incyte Clone No: 1393301

<400> 30

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<211> 768

<212> DNA

<213> Homo sapiens

<220>

<221> misc_feature

<223> Incyte Clone No: 1444055

<400> 31

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<210> 32

<211> 2069

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<223> Incyte Clone No: 1650177

<400> 32

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<211> 2594

<212> DNA

<213> Homo sapiens

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<223> Incyte Clone No: 1902576

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<213> Homo sapiens

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<211> 3080

<212> DNA

<213> Homo sapiens

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<210> 36

<211> 1154

<212> DNA

<213> Homo sapiens

<220>

<221> misc feature

<223> Incyte Clone No: 2588566

<400> 36

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<211> 2827

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 2811

<223> a or g or c or t, unknown, or other

<220>

<221> misc_feature

<223> Incyte Clone No: 2740570

<400> 37

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<211> 2987

<212> DNA

<213> Homo sapiens

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<221> misc_feature

<223> Incyte Clone No: 2820384

<400> 38

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 <213> Homo sapiens

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<210> 40
 <211> 1037
 <212> DNA
 <213> Homo sapiens

<220>
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